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OM protein - protein search, using sw model

June 9, 1999, 10:26:01; Search time 23.43 Seconds Run on:

(without alignments)
178.687 Million cell updates/sec

US-08-486-814-17 Perfect score:

1080 1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207 Sequence:

BLOSUM62 Scoring table: 162890 seqs, 20225328 residues Searched:

A_Geneseq_34:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	,	Describeron	transactiv	d type In-10 d	Type E.col	-chimeric	-chimeric t	rotein enc	ence of th	transac	tTAs transactivato	d pASK	line	tri	ransact	TAk enc	Tet repre	ed Tet r	ed Tet r	ed Tet r	ted Tet repre	ed Tet r	ed Tet repre	Tet repre	ed Tet 1	red Tet 1	ed Tet 1	Tn-1	ed Tn-1(reverse T	Tet repre	Tet repre	Tet repr	encoded	encod	Tet	Tet r	ated Tet	Н	ated Tet repre	ted Tet r	ted Tet r	ted Tet r	Mutated Tet repres	Mutated Tet repres
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Mutated Tet repres
Mutated Tet repres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Regulatory systems using tetracycline-controllable transactivator (tTA) - useful for conditional inactivation or modulation of gene expression in a host cell or animal bisclosure; page 46-48; 103pp; Bnglish coding for the C-terminal 130 amino acids of VP16 of HSV was blunted and inserted in pUHD14-1. The resulting plasmid, pUHD15-1, encoded a tetR-VP16 fusion protein, or tetracycline-controllable transactivator (tTA), whose sequence is Gequence 335 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUL-1996 (first entry)
Wild type Tn-10 derived Tet repressor.
Tet repressor; Herpes simplex virus; HSV; virion protein 16; VP16; fusion protein; gene expression; regulation; inhibition; activation;
                                                                                                                                                                                 tTA; transactivator; tetracycline-controllable transactivator; conditional inactivation; homologous recombination; gene expression; gene regulation; gene therapy; tetracycline-resistance; tetR; transgenic animal.

Herpes simplex virus K12, KOS.
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100.0%; Pred. No. 1.2e-112;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                     rd H, Gossen M, Salfeld JG, Voss JW;
95-036472/05.
                                                           ALIGNMENTS
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W08309
W08311
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                                                                                                                                  R64808 standard; Protein; 335 AA.
                                                                                                                                                              17-JUL-1995 (first entry)
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Matches 207; Conservative
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29-JUN-1995; U08179.
01-JUL-1994; US-270637.
                                                                                                                                                                                                                                                                                   22-DEC-1994.
14-JUN-1994; U06734.
14-JUN-1993; US-076327.
(BADI ) BASF AG.
   207
                                                                                                                                                                               tTA transactivator.
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   97.6
97.6
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R64808
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inhibit transcription

Glaim 38: Page 78: 112pp; English.

Fusion proteins comprising a first polypeptide which binds to a tet

Claim 38: Page 78: 112pp; English.

Fusion proteins comprising a first polypeptide which binds to a tet

coperator sequence in the presence of tetracycline or a tetracycline

analogue, operatively linked to a second polypeptide which either

activates or inhibits transcription in eukaryolic cells may be used

to activate or inhibit transcription in eukaryolic cells may be used

to activate or inhibit transcription. Such proteins may be used

to activate or inhibit transcription of gene products in transgenic

gene therapy and for expression of gene products in transgenic

cryanisms. Induction of gene expression is rapid, efficient and

strong, typically 1000-2000 fold. The inducing agent does not cause

strong, typically 1000-2000 fold. The inducing agent does not cause

cequence is the wild type Tn-10 tet repressor.

Sequence 207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory fusion protein - comprising modified tetracycline repressor able to bind mutant tet operator, fused to transcription repressor able to bind mutant tet operator, fused to transcription Example 4; page 84-85; 117pp; English.
W08295 represents wild-type Tet repressor (TetR) protein, derived from transposon 10 (Tn10) of E. Coli. The wild-type sequence is used for the production of a mutated TetR (e.g. so as to bind its target in the presence rather than the absence of tetracycline). Mutant TetR proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAR-1997 (first entry)
Wild-type E.coli In10-derived Tet repressor.
Tet; tetracycline; Tc; operator; transcription; regulation; inducible; repressor; gene expression; therapy; transgenic animal; disease model;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                   New tetracycline-regulated transcription modulators - comprising fusion proteins which bind to tet operator sequences to activate or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1080; DB 1; Length 207; 100.0%; Pred. No. 5.9e-113; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gossen M, Helbl V, Hillen W, Schnappinger D;
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Nucleic acid encoding tetracycline-inducible transcription
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15-JUL-1994; US-275876.
03-FEB-1995; US-383754.
07-JUN-1995; US-486814.
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07-JUN-1995; US-485971.
(BADI ) BASF AG.
                                                                                                    Bujard H, Gossen M;
WPI; 96-087666/09.
N-PSDB; T11351.
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                                                             (BUJA/) BUJARD H.
(GOSS/) GOSSEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
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can be fused to a transcriptional activator e.g. vp16 (herpes simplex virus virion protein 16), to form a Tc-controlled transcriptional activator (traf). The main invention of the specification concerns modified TetR proteins that bind to modified class B tet operator concerns are teto-4C and teto-6C (see T45711 and T48478). Modified TetR proteins can be fused to any transcription regulatory polypeptide and used to control transcription of a teto-4C or teto-6C linked gene. Nucleic acid encoding such a fusion protein may be introduced into a call and transcription of the protein can be controlled by altering the conce. of tetracycline (or an analogue) in the cell, as appropriate. This ability to modulate gene expression in a predictable way is very useful in gene therapy and for recombinant protein prodn. in cultured cells or transgenic animals. The Tc-inducible system is also useful for the prodn. of transgenic animal models for the study of disease and also for the study of gene function e.g. during differentiation. The concent cellular toxicity, high concns. of inducer are not required.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New packaging cell lines for pseudotyped retroviral vectors comprises sequences encoding retroviral Gag and Pol polypeptide(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig. 94.07. 84pp; English.
This fusion protein comprises a multi-chimeric transactivator,
designated rTAER, that is composed of (from the N-terminus to the
C-terminus) the Escherichia coli tetR polypeptide, the
transcriptional activation domain of herpes simplex virus VP16, an
the ligand binding domain of the oestrogen receptor. An inducible
expression system of the invention is composed of tTAER and a
                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 100.0%; Score 1080; DB 1; Length 207; Local Similarity 100.0%; Pred. No. 5.9e-113; les 207; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multi-chimeric transactivating factor rTAER fusion protein.
Multi-chimeric transactivating factor; rTAER; tetR;
tetracycline repressor; HSV; oestrogen receptor; promoter;
packaging cell line; retrovirus; retroviral particle; vector;
gene delivery; gene therapy.
Chimeric - Bscherichia coli.
Chimeric - Herpes simplex virus.
Chimeric - Mammalia.
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Whis '8-145602/13.

N-PSDB; V17756.
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07-AUG-1996; US-694652.
(CITX ) CITY OF HOPE.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and envelope protein
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transcriptional activation. Sequence 651 AA;

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New inducible expression systems - comprising multi-chimeric
New inducible expression systems - comprising multi-chimeric
Transactivator, induces transcription from promoter in the absence
of first ligand and presence of second ligand
Frample 1; Fig 4; 72pp; English.

Example 1; Fig 4; 72pp; English.

This is a fusion protein comprising, from N-terminus to C-terminus,
the E.coli tetR polypeptide, the transcription activational domain
the E.coli tetR polypeptide, the transcription activational domain
of HSV VPI6 and the ligand binding domain of an oestrogen receptor
from pHE14 (Kumar et al. 1986). DNA encoding it can be used as part of
an inducible expression system which induces transcription from the
promoter in the absence of the first ligand and presence of the
second. The products can be used for the inducible expression in cells
of polypeptides such as cytotoxic products or therapeutic products.
The activation of the inducible expression system requires 2
independent signals, which reduces the incidence of undesired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
minimal promoter (see V17755) derived from the immediate early gene
of cytomegalovirus linked to 7 tandem copies of the tet operator
(teto) that is the binding site for tetk, which in turn can be
linked to a nucleotide sequence of interest. The invention relates
to packaging cell lines derived from Helax, D17, MDCK, BHK or
preferably (f271 cells and recombinant retroviral particles.
produced by them, particularly pseudotyped retroviral particles.
Retroviral particles are produced by inducibly expressing an
envelope protein by linking an envelope protein-encoding nucleotide
sequence to the inducible expression in cells of polypeptides, e.g.
cytotoxic products or therapeutic agents. The activation of the
inducible expression system. The activation of the
inducible expression system requires 2 independent signals, thus
reducing the indicence of undesired transcriptional activation.
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WPI; 98-145597/13.
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07-AUG-1996; US-693940.
(CITY ) CITY OF HOPE.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ligand-binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Claim 4; Columns 77-80; 63pp; English.

Claim 4; Columns 77-80; 63pp; English.

Crap present sequence is encoded by wild type Tn10-derived tet repressor.

It is used in the course of the invention. The specification describes a control of a subject. The method comprises introducing into the control of a subject. The method comprises introducing into the coll a nucleic acid encoding a fusion protein which inhibits transcription in eukaryotic cells, the fusion protein comprising a control of properties which inhibits transcription in eukaryotic cells and modulating the concentration of a tetracycline expression system, using tetracycline (analogue) in the subject. The method is used for the regulation of canalogue) in the subject. The method is used for the regulation of canalogue in the subject of the system to be induced in the presence of canalogue 207 AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                     61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                      1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetracycline based regulation of gene expression - uses a tetracycline operator sequence joined to a gene of interest, the gene of interest being induced in the presence, but not absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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   Length 651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-1998 (first entry)
protein encoded by wild type Tnl0-derived tet repressor.
Tet repressor; tetracycline; regulation; expression;
Tet operator-linked gene; tet operator.
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1080; DB 1;
100.0%; Pred. No. 5.9e-113;
tive 0; Mismatches 0;
100.0%; Score 1080; DB 1; 100.0%; Pred. No. 2.9e-112;
                                                                ö
                       100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W71326 standard; Protein; 207 AA.
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Best Local Similarity 100.0
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995; US-485978.

07-JUN-1995; US-485978.

14-JUN-1993; US-076327.

14-JUN-1994; US-260452.

01-JUL-1994; US-270637.

15-JUL-1994; US-278976.

06-FEB-1995; US-3783754.

(RNOL.) KNOLL AG.
                                                                   Matches 207; Conservative
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                                           Similarity
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             Query Match
                                               Best Local
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(first entry)

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17-JUL-1995
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                                                           61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                           121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                        1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                             Tetracycline repressor-mediated regulation system - useful for controlling gene expression in transgenic animals
Disclosure; page 41-42; 76pp; English.
The inventors claim a construct which comprises an animal promoter element having a tetracycline repressor (tetR) operator. The promoter element may be the PEPCK promoter which is tissue specific shortly prior to birth. The tetR sequence in the construct is 3' to a TATA-box sequence and is inserted into the NheI site of the PEPCK promoter element. The entire sequence of the tetR Sequence 207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                          19-AuG-1994 (first entry)
Sequence of the tetracycline repressor tetR.
Tetracycline repressor; TetR; In10; transposon 10.
                                                                                                                                       181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                    181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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                                                                                                                                                                                                                    R48630 standard; Protein; 207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R64809 standard; Protein; 297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 206; Conservative
                                                                                                                                                                                                                                                                                                             26-AUG-1993; UO8230.
26-AUG-1992; US-935763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                          94-083191/10.
                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                     (DNXD-) DNX CORP.
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                                                                                                                                                                                                                                                                                        WO9404672-A.
                                                                                                                                                                                                                                                                                                    03-MAR-1994.
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WPI; 94-0
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tTA; tTAS; transactivator; tetracycline-controllable transactivator; conditional inactivation; homologous recombination; gene expression; gene regulation; gene therapy; tetracycline-resistance; tetR; transgentc animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DRHHTHECPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulatory systems using tetracycline-controllable transactivator (TTA) - useful for conditional inactivation or modulation of gene expression in a host cell or animal bisclosure; Page 50-51; 103pp; English.
A DAM fragment of pwsypl6 coding for the C-terminal 97 amino acids of VP16 of HSV was blunted and inserted in pw1014-1. The resulting plasmid, pu10151-1, encoded a tetR-VP16 fusion protein, or tetracycline-controllable transactivator (smaller version, tTAs), sequence 197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide encoding trans:activator fusion protein contg. tet repressor - used to control expression of gene regulated by minimal promoter linked to tet operon, and vectors and cells where gene expression is regulated by tetracycline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tTAS transactivator.
Transactivator; tTAS; tet repressor; tetR; virion protein 16; VP16; gene expression; tetracycline-responsive promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.5%; Score 1075; DB 1; Length 297; 99.5%; Pred. No. 3.5e-112; tive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                  (BADI ) BASF AG.
Bujard H, Gossen M, Salfeld JG, Voss JW;
WPI: 95-016472/05.
N-PSDB; Q76265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R85324 standard; Protein; 297 AA.
                                                                                                  Herpes simplex virus K12, KOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic animal.
Chimeric Escherichia coli;
Chimeric Herpes simplex virus.
USS464758-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206; Conservative
                                                                                                                                                  22-DEC-1994.
14-JUN-1994; UO6734.
14-JUN-1993; US-076327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0/-NUV-1995.
14-JUN-1993; 076726.
14-JUN-1993; US-076726.
tTAs transactivator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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WPI; 95-392612/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BUJA/) BUJARD H.
(GOSS/) GOSSEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T06868.
                                                                                                                        WO9429442-A.
                                                                                                                                           22-DEC-1994
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A fusion protein (R85324) composed of the Escherichia coli Th10 tet repressor (tetR) and a 127-amino acid C-terminal portion of the transcription activating domain of herpes simplex virus virion protein 16 (VP16) is the product of novel tetracycline-controlled transactivator tTA (T06869). The transactivator is used to regulate expression of a heterologous gene operably linked to a minimal promoter derived from human cytomegalovirus promoter IE (see T06899-70) and at least 1 tet operator (tetQ) sequence. On/off regulation of expression of the heterologous protein by host eukaryotic cells is provided by varying the medium tetracycline conc. Transgenic animals producing sequence 297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prokaryour vector for regulated prodn. of heterologous protein gene controlled by promoter repressed by tetracycline repressor protein, prodn. of which is controlled by independent promoter not regulated by this repressor.

Disclosure: Fig la; 50pp; German.

Plasmid pARNT5 is a specifically claimed example of a prokaryotic expression vector comprising the tetracycline promoter/operator (P/O) region and the tetracycline repressor (tetR) gene. The tetR gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                        1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPILYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCOUNTING PASK75 open reading frame (c) translation.
Plasmid pASK75 open reading frame (c) translation.
Petracycline; resistance; TetR gene; repressor protein; TetA gene;
prokaryotic expression vector; beta-lactamase promoter; bla gene;
circular; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "each X corresponds to a termination codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C-terminal end of beta-lactamase; the exact position of the N-terminus is not given in the specification"
                                                                                                                                                                                                                                                                        99.5%; Score 1075; DB 1; Length 297; 99.5%; Pred. No. 3.5e-112; tive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-1894; DE-417588.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
Skerra A, Wardenberg C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          614. .820 - -
/label- TetR
/note= "tetracycline repressor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= OmpA_leader
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/note= "e
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                                                                                                                                                                                                                                                                                                                  Matches 206; Conservative
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                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                    297 AA;
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                                                                                                                                                                                                                        Sequence
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Example 2; Fig 8; 65pp; English.

This transactivator protein is encoded by a hybrid gene consisting of the tetracycline repressor gene (tetR) of E. coli (174611) fused in frame with the immediate early promoter (TEIA) of baculovirus (T74614). The protein is used to demonstrate a novel method of gene expression regulation of recombinant baculoviruses in an insect cell/host. An insect cell is constructed having a chimeric gene, which consists of a promoter (e.g. T74614) operably linked to DNA encoding a regularory protein capable of affecting gene expression. The regulatory protein capable of affecting gene expression. The regulatory protein capable of affecting gene expression. The regulatory protein capable of actions the second of the combinant baculovirus expression vector is then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             under the control of the heta-lactamase (bla) promoter. Expression of heterologous genes inserted downstream of the tet P/O is controlled by the activity of the Tet repressor. Plasmid pASK75 was derived from pASK60-Strep (Schmidt and Skerra, Frotein. Eng. 6 (1993), 109-122) and further contains the OmpA leader peptide coding sequence, a polylinker and a strept#tidin-binding peptide strep-tag coding region from the parent plasmid. In addition, pASK75 contains the ColEl origin of replication, the bla geit, ihrergene regions of filamentous phage fl and a lipoprotein terminator. The specification includes the translated sequences from all three regions are all in reading frame (C).
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    using recombinant

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                                                                                                                                                                                                                                                                                                      Length 1088;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetracycline transactivator fusion protein tetrIEIA.
Baculovitus, recombinant protein, neurotoxin; parasite;
biological control; insecticide; insecticidal protein;
nuclear polyhedrosis virus; early promoter; tetracycline.
                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                      99.5%; Score 1075; DB 1; 99.5%; Pred. No. 2.2e-111;
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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/label= "tetR peptide"
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/label= "IElA peptide"
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22-DEC-1995; US-009120.
(DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Escherichia coli.
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W21994 standard; Protein; 354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W21994;
26-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.58
Matches 206; Conservative

    Baculovirus.

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16-DEC-1996; U20512.
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us-08-486-814-17.rag

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constructed. This has a second chimeric gene, which consists of a promoter (one or more tetracycline operator sites operably linked to a minimal promoter region, see T14615-16) that is affected by the above regulatory protein. This promoter is operably linked to DNA encoding an insecticidal protein, (W21993). The recombinant baculovirus expression fusects is introduced into the recombinant insect cell. Expression of the recombinant insect cells and the recombinant baculoviruses may be used in the production of insecticidal recombinant baculoviruses may be used in the production of insecticidal recombinant baculoviruses. Insect cells treated with recombinant viruses, as described, show an increase in the Sequence 354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
         893688888888888
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ó; 121 CQGGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180 61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120 0; Gaps 1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60 99.5%; Score 1075; DB 1; Length 354; 99.5%; Pred. No. 4.5e-112; 1ve 0; Mismatches 1; Indels (181 GAEPAFLFGLELIICGLEKQLKCESGS 207 181 GAEPAFLFGLELIICGLEKOLKCESGS 207 Best Local Similarity 99.5 Matches 206; Conservative g ò g δλ g ò

MEDICAL MEDICALE AG.
Bruhn H. Fruk M. Henkel T. Steipe B;
WPI; 98-230215/20.
WPI; 98-230215/20.
Vectors used to produce PH domain-like peptide libraries - which are screened for therapeutically useful peptide(s), e.g. to produce Example 4; Page 79-81; 137pp; English.
This polypeptide comprises a fusion between a synthetic Pleckstrin homology (Phi) domain (see W34285) of human cytohesin 1 and a tet repressor. It is encoded by plasmid pTLP2 (see V36524). The fusion protein is expressed from a polycistronic message, constitutively transcribed from the beta-lactanase promoter. The plasmid was used to transform Escherichia coli JM109 cells. The construct was used to demonstrate the folding, stability, functionality and ease of handling of a fusion protein comprising a synthetic PH domain and 28-AUG-1998 (first entry)
Pleckstrin homology domain-tet repressor fusion.
Pleckstrin homology domain; PH domain; peptide library;
functional molecular surface; protein structural template;
vaccine; gene therapy; cytohesin 1; human; plasmid pTLP2; .221
 /label= Tet_repressor Location/Qualifiers /label= PH_domain W54311 standard; Protein; 349 AA. Chimeric - Homo sapiens. Chimeric - Escherichia coli. 30-MAY-1997; E02840. 31-MAY-1996; EP-108776. WO9745538-A1. 04-DEC-1997 Synthetic. Protein Protein RESULT 12 W54311 g

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Gaps

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Score 1073; DB 1; Length 335; Pred. No. 7e-112; 0; Mismatches 1; Indels (

99.4%;

Matches 206; Conservative

Query Match Best Local Similarity

Polynuciactide encoding transfactivator fusion protein contg. tet Polynuciactide encoding transfactivator fusion protein contg. tet repressor - used to control expression of gene regulated by minimal promoter linked to tet operor, and vectors and cells where gene expression is regulated by tetracycline and cells where gene piscolosure; Fig 4A-B; 37pp; English.

A fusion protein (R85323) composed of the Escherichia coll Thio tet repressor (tetR) and a 127-amino acid C-terminal portion of the transcription activating domain of herpes simplex virus virion transactivator tita (VPIG) is the product of novel tetracycline-controlled transactivator transport or cytomegalorize promoter is used to regulate expression of a heterologous gene operably linked to a minimal promoter derived from human cytomegalorizus promoter is (see T06869-70) and at least 1 tet operator (tetC) sequence. On/off regulation of expression of the heterologous protein by host eukaryotic cells is provided by varying the medium tetracycline conc. Transgenic animals producing a desired protein in their milk can also be produced. 62 DRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 121 61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120 121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180 0; Gaps 2 MSKLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 61 a DNA binding domain. The invention provides vectors that are used for the production of PH domain-like peptide libraries, which can be screened to identify peptides that have desirable properties, especially novel binding or catalytic properties, and which may be of use in research or therapy, or as vaccines. Novel synthetic protein structural templates for the generation, screening and evolution of functional molecular surfaces are provided. Sequence 349 AA; 1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML Transactivator; tTA; tet repressor; tetR; virion protein 16; VP16; Length 349; 1; Indels gene expression; tetracycline-responsive promoter; 99.5%; Score 1075; DB 1; 99.5%; Pred. No. 4.4e-112; iive 0; Mismatches 1; GAEPAFLFGLELIICGLEKQLKCESGS 207 182 GAEPAFLFGLELIICGLEKQLKCESGS 208 R85323 standard; Protein; 335 AA. Chimeric Escherichia coli; Chimeric Herpes simplex virus. 13-MAR-1996 (first entry) tTA transactivator. Matches 206; Conservative US5464758-A. 07-NOV-1995. 14-JUN-1993; 076726. 14-JUN-1993; US-076726. Bujard H, Gossen M; WPI; 95-392612/50. Best Local Similarity transgenic animal (BUJA/) BUJARD H. (GOSS/) GOSSEN M. N-PSDB; T06867. Query Match RESULT 13 R85323 181 888888888 ò ŏ a ò q á g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 RHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFLC 121
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                                                                   2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLD 61
1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; 14987.

Nucleic acid encoding tetracycline transactivator fusion protein routoleic acid encoding tetracycline transactivator fusion, e.g. for creating animal models for drug screening farmal models for drug screening animal models for drug screening farmal models for drug screening farmal models for for for farmal it. Fig. 10b-g; 82pp. English.

Autoregulatory plasmid pret-trak (149877) contains a modified tetracycline transactivator gene, trak, under control of a minimal promoter. It encodes a 36c-mino acid protein (M9874). An autoregulatory tetracycline-regulated system for inducible gene expression in eukaryotes has been developed that allows the rapid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reversible control of gene expression in eukaryotic cells, and creation of transgenic animals in which expression of a luciferase reporter gene is controlled by altering the concentration of tetracycline in the drinking water of the animals.
               121 COOGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ
                                                                                                                                                                                                                                                                                                     pret-trak encoded protein.
pret-trak; pret-Splice; tetracycline transactivator; promoter;
pret-trak; pret-Splice; tetracycline transactivator; promoter;
gene expression; transgenic animal; animal model; drug screening.
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99.1%; Score 1070; DB 1; Length 336;
Best Local Similarity 99.5%; Pred. No. 1.5e-111;
statches 205; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                              181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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                                                                                                                                                                                                                                                             W08474 standard; Protein; 336 AA
                                                                                                                                                                                                                                                                                        28-MAR-1997 (first entry)
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07-JUN-1995; US-474169.
(UYXA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 97-077273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 AA;
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Nucleic acid encounts terracycine-inducible remuscription
regilatory fusion protein - comprising modified tetracycline
regressor able to bind mutant tet operator, fused to transcription
regilator, useful for modulating eukaryotic gene expression
Claim 5: Page -: ilTpp: English.
Claim 5: Page -: ilTpp: English.
Common tetracycline for modulating eukaryotic gene expression
CC transcriptional control sequence (e.g. v-rchA silencer domain), to
transcriptional control sequence (e.g. v-rchA silencer domain), to
The main invention of the specification concerns modified TetR proteins
CC that bind to modified class B tet operator sequences tetO-4C and
teto-6C (see T45711 and T48478). Modified TetR proteins can be fused
to any transcription regulatory polypeptide and used to control
transcription of a tetO-4C or tetO-6C linked gene. Nucleic acid
croding such a tetO-4C or tetO-6C linked gene. Nucleic acid
transcription of the protein may be introduced into a cell and
transcription of the protein may be introduced into a cell and
tetracycline (or an analogue) in the cell, as appropriate. This
ability to modulate gene expression in a predictable way is very useful
conformation of the Te-combinant protein produ. in cultured cells or
in gene therapy and for recombinant protein produ. in cultured cells or
transgenic animals. The Tc-inducible system is also useful for the
for the study of gene function e.g. during differentiation. The
for the study of gene function e.g. during differentiation. The
common components of inducer are not required.
Common common components of inducer are not required.
Common components.
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Mutated Tet repressor for Tet-inducible transcriptional regulator.
Tet; tetracycline; Tc; operator; transcription; regulation; inducible; repressor; gene expression; therapy; transgenic animal; disease model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding tetracycline-inducible transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rd H, Gossen M, Helbl V, Hillen W, Schnappinger D;
97-052305/05.
                                                                                                                                                                                                                                                                                              /note= "Lys replaces wild-type Glu" misc_difference 39
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Gln replaces wild-type Pro"
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                                                                                                                                                                                                                                                                                                                                                                                             /label= substitution
                                                                                                                                                                                                                                     Location/Qualifiers
W08323 standard; Protein; 207 AA.
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Best Local Similarity 99.03
Matches 205; Conservative
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                                                                                                                                                                                                                                                                     misc_difference 3
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                                      W08323;
21-MAR-1997
                                                                                                                                                                                                             Synthetic.
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RESULT

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

June 9, 1999, 10:27:01; Search time 19.42 Seconds (without alignments) 399.294 Million cell updates/sec

1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207 US-08-486-814-17 1080 Perfect score: Sequence:

BLOSUM62 Scoring table: 116738 segs, 37460341 residues Searched:

PIR_58:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	repressor tetR - 1	atory protei	. prote	ne resi	e re	prote		or	r pro	Д	o	hypothetical prote	probable transcrip	ر. ت	transcription regu	transcription regu	hypothetical prote	glucuronide repres	hypothetical prote	n reg	ical p	3	transcription regu	conserved hypothet	ndent	cal	call	nse	n reg	prot	l prot	_	yen fixati	prote	in -	2	ical pro	probable arginyl-t	transcription regu
SOMMAKIES	ΙD	RPECT	S07359	S30287	A26948	RPECYS	JQ1478	S38655	177569	RPECR1	H70740	A40046	A69900	S42417	S42419	H70042	C70487	B70827	D64918	875298	B70391	E70861	F70946	C70035	A64695	E69280	S29308	D64855	I49045	E69779	S12393	H70001	C70649	S31136	S10899	S17885	F70487	F64995	A71023	S39744
	DB	-																																						
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æ	Query Match	. 66	ë.	ë,	7.	ω.	ζ.	7.	ζ.	ė.		ë.	ä	ö	ö	ö	6																				7.7			
	Score	107	m	ന	-	22	'n.	'n.	ď	'n.	176.5	ė,	Ξ	10.	10.	œ.	20	96	'n	94.5	94	93.5	٠.	88	87.5	Ġ	86	85.5	'n	85	84	84	83.5		83	83	83	82	-	81.5
	Result No.		7	m	4	Ŋ	ب	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	. 37	38	39

nitrogen fixation hypothetical prote ttk protein - Esch hypothetical prote probable transcrip repressor for cyto
S19883 S58095 C65165 S38906 E70873 A42116
000000
517 543 212 190 187
2.7.7. 2.4.7.7. 3.3.4.5.
80.5 80.5 80 80 80 79
44444 01128444 2433

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Ny Alternate names: tet repressor class D
C; Species: Bscherichia coli
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 12-Jun-1998
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 12-Jun-1998
C; Accession: S07359
R; Unger, B.; Klock, G.; Hillen, W.
Nucleic Acids Res. 12, 7693-7703, 1984
A; Title: Nucleotide sequence of the repressor gene of the RAI tetracycline resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory protein tetR - Escherichia coli plasmid RA1
                                                                repressor tetR - Escherichia coli transposon Tn10
ALIGNMENTS
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181 DGEQAFLHGLESLIRGFEVQL 201
              181 GAEPAFLFGLELIICGLEKQL 201
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Matches 119;
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Best Local 8
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**Alard, J.D.; Gibson, M.L.; Vu, L.H.; Nguyen, T.T.; Bertrand, K.P.

Mol. Gen. Genet. 237, 301-305, 1993

**Title: Nucleotide sequence of class D tetracycline resistance genes from Salmonella or A; Reference number: $30286

**Accession: $30287

**Molecule type: DNA

**Residence: EMBL: X65876; NID:949073; PID:949075
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N.Alternate names: tetracycline repressor
C;Species: Salmonella ordonez
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                          61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                      A Genome: plasmid
C:Superfamily: tetracycline repressor
C:Keywords: antibiotic resistance; DNA binding; transcription regulation
F:25-46/Region: helix-turn-helix *status predicted
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                                                                  A;Cross-references: EMBL:X01083; NID:g43053; PID:g43054
C;Genetics:
A;Gene: tetR
                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                              Query Match
63.2%; Score 683; DB 2;
Best Local Similarity 65.2%; Pred. No. 4.1e-56;
Matches 131; Conservative 26; Mismatches 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.2%; Score 683; DB 2;
65.2%; Pred. No. 4.1e-56;
Live 26; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Gene: tetR
A Genome: plasmid
C Superfamily: tetracycline repressor
C; Keywords: antibiotic resistance; DNA binding; tre
F; 25-46/Region: helix-turn-helix #status predicted
Reference number: S07359; MUID:85037938
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Matches 131; Conservative
                                                  A; Residues: 1-218 <UNG>
                                      A; Molecule type: DNA
                    S07359
                    A; Accession:
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C.Species: Haemophilus parainfluenzae
C.Species: Haemophilus parainfluenzae
C.Species: Haemophilus parainfluenzae
C.Species: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 12-Jun-1998
C.Species: 10-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 12-Jun-1998
C.Species: Hickman, R.K.; Curiale, M.S.; Hillen, W.; Levy, S.B.
J. Bacteriol. 169, 990-994, 1987
A.Title: Constitutive expression of tetracycline resistance mediated by a Tn10-like A.S. Reference number: A26948; MUID:87137315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M36272; NID:g150945; PID:g150946
C;Comment: This protein is the repressor of the tetracycline resistance element; its
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Escherichia coli
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 12-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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tetracycline resistance protein - Haemophilus parainfluenzae
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                                                                                                                                                                                                                                                                             A.Molecule type: DNA
A.Residues: 1-126 <HEU>
A.Cross-references: GB:M15539; NID:g148988; PID:g148989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.3%; Score 619; DB 2; L6
95.2%; Pred. No. 1.7e-50;
live 1; Mismatches 5;
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C;Superfamily: tetracycline repressor
F;25-46/Region: helix-turn-helix #status predicted
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C.Superfamily: tetracycline repressor
C.Superfamily: tetracycline reststance; DNA binding; tran
F.24-46/Domain: DNA binding #status predicted C.24-66/Region: helix-turn-helix #status predicted
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Mol. Biol. Evol. 2, 1-12, 1985
A.Title: The tetracycline repressor of psc101.
A.Reference number: A03575; MUID:88216101
A.Molecule type: DNA
A.Residues: 1-219 < BRO>
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Mol. Gen. Genet. 215, 76-80, 1988
A; Title: Identification and nucleotide sequence of the class E tet regulatory element A; Reference number: I57766; MUID:89201249
A; Accession: I77569
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C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 12-Jun-1998
C;Accession: I77569
R;Tovar, K.; Ernst, A.; Hillen, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                              Length 216;
                                                                                                               A;Cross-references: EMBL:X75761; NID:g415984; PID:g415985
C;Superfamily: tetracycline repressor
F;25-46/Region: helix-turn-helix #status predicted
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A) Residues: 1-211 <RES>
A) Cross-references: EMBL:X14035; NID:943055; PID:943056
C) Superfamily: tetracycline repressor
F;25-46/Region: helix-turn-helix #status predicted
                                                                                                                                                                                                                                         Query Match 47.7%; Score 515.5; DB 2; Best Local Similarity 52.5%; Pred. No. 1.3e-40; Matches 106; Conservative 33; Mismatches 60;
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A; Reference number: S38655
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Best Local Similarity
                                                                       A; Molecule type: DNA
A; Residues: 1-216 < TRU>
                                               A; Status: preliminary
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                          A; Accession: S38655
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A; Residues: 1-216 <ALL).
A; Residues: 1-216 <ALL).
A; Residues: 1-216 <ALL).
A; Cross-references: EMBL:X61367; NID:948194; PID:948198
A; Cross-references: EMBL:X61367; NID:948194; PID:948198
B; Altschmied, L.; Baumeister, R.; Pfleiderer, K.; Hillen, W.
EMBO J. 7, 4011-4017, 1988
A; Title: A threonine to alanine exchange at position 40 of tet repressor alters the reccategory.
A; Reference number: S02667; MUID:89091153
A; Accession: S02668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 12-Jun-1998
C;Accession: JO1478; S02668; S24113
R;Allmeier, H.; Cresnar, B.; Greck, M.; Schmitt, R.
Remelli, 11-20, 1992
A;Title: Complete nucleotide sequence of Tn1721: gene organization and a novel gene prod
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Jun-1998
C;Accession: S38652
R;Trueman, P.; Sharpe, G.S.; Barth, P.T.
submitted to the EMBL Data Library, November 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                            61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                          121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERE----TPTTDSMPPLLRQAIEL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 47.7%; Score 515.5; DB 2; Length 216; Best Local Similarity 52.5%; Pred. No. 1.3e-40; Matches 106; Conservative 33; Mismatches 60; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                     regulatory protein tetR - Escherichia coli transposon Tn1721
N;Alternate names: tetracycline resistance repressor
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: tetracycline repressor
F;25-46/Region: helix-turn-helix #status predicted
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A; Residues: 1-100 <ALT>
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tet repressor protein (Tn 1721) - Escherichia coli plasmid RP1 C;Species: Escherichia coli C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 12-Jun-1998	chmitt, R.	C.Genetics: A.Gene: tetR A.Gene: plasmid C.Superfamily: tetracycline repressor C.Superfamily: tetracycline r	Query Match Best Local Similarity 51.5%; Score 505.5; DB 1; Length 216; Best Local Similarity 51.5%; Pred. No. 1.1e-39; Matches 104; Conservative 34; Mismatches 61; Indels 3; Gaps 2; QY 1 MSRLDKSKVINSALELLEVGIEGLTTRILAGKLGVEQPTLXWHYKNRALLDALAIEML 60	QY 61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120 : - - - - - - - - - - - - -	<pre>4y 121 COOGESLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFD 178 : : : : </pre>	C; 179 HQGAEPAFLFGLELIICGLEKQ 200 : : : bb 180 EAGPDAAFEGGLAVIVDGLAKR 201	RESULT 10 H70740	A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987 A;Reference number: A70740 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-261 <col/> A;Residues: 1-261 <col/> A;Residues: 1-261 <col/> A;Residues: 1081 <col/> A;Residues: 10		LDKSKVINSALELLENEVGIEGLTTRKI LDKSKVINSALELLENEVGIEGLTTRKI

155 DDLDKETAVIF 165

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C;Date: Ub-Dec-199/ #sequence_revision Ub-Dec-199/ #text_Cnauge 44-Sep-1990
C;Accession: H70042
R;Kunst, F: Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R;Kunst, F.; Ogasawara, N.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Birlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A;Authors: Fritz, C.; Pujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Gh A;Authors: Fritz, C.; Fujita, M.; Fujita, K.; Lapidus, A.; Lardinois, S.; Laube Konigstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Lardinois, S.; Laube Konigstein, G.; Krogh, S.; Fark, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Por K.; Ogiwara, A.; oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Por K.; Cir, Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schlavotta, C.; Roche, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schlavotta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schlavotta, C.; Ruston, T.; Terpstra, P.; Tespunoi, A.; Tosato, V.; Uchiyama, S.; Vanden, M.; Authors: Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama, S.; Vashikawa, A; Reference number: A69580; MUID:98044033
A; Reference number: A69580; MUID:98044033
A; Reference number: Person Reviews A14 Pooley Reviews A14 P
                                                                                                                                                                                                                C. Species: Neisseria gonorrhoeae
A; Variety: strain FA19
C; Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
B; Pan, W.; Spratt, B.G.
Mol. Microbiol. 11, 769-775, 1994
A; Title: Regulation of the permeability of the gonococcal cell envelope by the mtr sy A; Reference number: S42417
A; Reference number: S42417
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998
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                                                                                                                                                                                       probable transcription repressor mtrR - Neisseria gonorrhoeae (strain FA19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 ----HFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFLC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%; Score 110.5; DB 2; Length 210; 27.4%; Pred. No. 0.0035; Live 22; Mismatches 73; Indels 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:225797; NID:9452332; PID:9438189
A;Experimental source: strain FA19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: mtrR
C; Superfamily: probable transcription repressor mtrr
C; Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown
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Best Local Similarity
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A; Residues: 1-210 <PAN>
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Mol. Microbiol. 11, 769-775, 1994
A; Title: Regulation of the permeability of the gonococcal cell envelope by the mtr systel. Reference number: $42417
A; Accession: A69900
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Rossidues: 1-191 - KVUN>
A; Construction outce: strain 168
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIE---LF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 CEH--TEQNA--AVIAIA------RKHQAIWREKIT------AVLTEAVENQDLA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 LDRHHTHFCPLEGES------WQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 TLENQLAFICQQGFSLENALYALSAVGHFTLG--CVLEDQEHQVAKE--ERETPTTDSMP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 FDQMADSVIERKGDSAMLSLAHAYVDFAIENPGYYEAALL-----KVH-----DKRTE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 119; DB 2; Length 191;
23.6%; Pred. No. 0.00051;
tive 39; Mismatches 74; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LIQKMIVDAAAEIADQEGVNGVSLAALSKKMNVRPPSLYNHINGLQAIRAELAVRGLIKL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAI----EM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h
Similarity 27.2%; Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73;
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S.Superfamily: probable transcription repressor mtrr
C.Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 FSIR-----TFLSGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 PLLRQAIELFDHQGAEPAFLFGL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 DHQGAEPAFLF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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A; Residues: 1-210 <PAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S42417
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Best Local S
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Best Local S
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Gaps

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A;Cross-references: GB:Z99122; GB:AL009126; NID:g2636029; PID:e1184426; PID:g2636046
A;Experimental source: strain 168
C;Genetics:
A;Gene: yvkB
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2
                                                                                                                                                                                                        63 HHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFLCQ 122
                                                                                                                                                                                                                                                                 123 QGFSLENALYALSAVGHFTLGCVLEDQEHQ-------VAKEERETPTTDSM 166
                                                                                    Ouery Match
Best Local Similarity 19.6%; Pred. No. 0.0047;
Matches 41; Conservative 32; Mismatches 51; Indels 85; Gaps
                                                                                                                                                                                                                                                                                     3 RLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDR 62
                                                                                                                                                                 167 PPLLRQAIELFDHQG-----AEPAFLF 188
                                                                                                                                                                                                                                                                                                                                              120 KQLLVDYLKTMGEKGVIQTGNEAEHADVF 148
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Search completed: June 9, 1999, 12:59:50 Job time: 9169 sec

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GenCore version 4.5
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- protein search, using sw model OM protein

June 9, 1999, 10:29:01; Search time 16.52 Seconds (without alignments) 336.316 Million cell updates/sec Run on:

US-08-486-814-17

1080 Perfect score:

1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207 Sequence:

BLOSUM62 Scoring table: 74019 seqs, 26840295 residues Searched:

SwissProt_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		P04483 escherichia	pasteur	scheri	Polobi pasteurella	P03039 escherichia	escherichi	escheri	P51560 vibrio angu	Q11023 mycobacteri	P39897 neisseria g	esc	Q60649 mus musculu	P75952 escherichia	P23217 staphylococ	P17446 escherichia	azotoba	P27598 ipomoea bat	escherich		schi		escheric	P43506 bacillus me	Q05870 schistosoma	P44907 haemophilus	esche		esche			S	o)	gallu		schiz		haemophil	droso	homo	schis	P40064 saccharomyc	Ē	P03959 escherichia
SUMMARIES		~l	- 1	ᆈ.	- 1	- 1	- 1	TER5_ECOLI	TER7_VIBAN	YO7H_MYCTU	MTRR_NEIGO	UIDR_ECOLI	SKD3_MOUSE	YCFQ_ECOLI	YP23_STAAU	BETI_ECOLI	NIFL_AZOVI	PHSL_IPOBA	YFAX_ECOLI	YWFK_BACSU		FA8_PIG	TTK_ECOLI	BM3R_BACME	MYSP_SCHJA	VACB_HAEIN	ACRR_ECOLI	SPCN_HUMAN	TRC5_ECOLI	YCDC_ECOLI	FA8_MOUSE	YD86_SCHPO	ENVR_ECOLI	HS9A_CHICK	KINH_HUMAN	YDH6_SCHPO	TTK_HAEIN	Y893_HAEIN		HS9B_HUMAN	MY SP_SCHMA	N157_YEAST	TIPO MOUSE	ECO
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P12758 escherichia P16749 human cytom	
UDP_ECOLI IE63_HCMVA	
252 744	
6.9 6.9	
74.5	
44 45	

ALIGNMENTS

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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89094871.

MEDLINE; 89094871.

J. MOL. BIOL. 203:949-959(1988).

ELEMENT: ITS AMINO-TERRINAL REGION FORMS A HELIX-TURN-HELIX STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE (TETA) PROMOTER OPERATOR SITES.

J. SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T->I: REDUCES AFFINITY FOR TETRACYCLINE
LESS THAN 10 FOLD.
4AB4DD5A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H->Y: REDUCES AFFINITY FOR TETRACYCLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REDUCES AFFINITY FOR TETRACYCLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.5%; Score 1075; DB 1; Length 207; Best Local Similarity 99.5%; Pred. No. 5.6e-93; Matches 206; Conservative 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAGNESIUM (OF [MG-TC]+ COMPLEX)
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X00694; G43052; -.

EMBL, J01830; G154846; -.

PIR, A03576; RPECTN.

PROSITE; PS01081; HTH_TETR_FAMILY; 1.

TRANSCRIPTION REGULATION; REPRESSOR; TRANSPOSABLE ELEMENT;

DNA-BIND C 26 45 H-T-H MOTIF (POTENTIAL).
                         13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS B (TRANSPOSON TN10).
                                                                                                                                                                                                                             MEDLINE; 84005886.
BERTRAND K.P., POSTLE K., WRAY L.V. JR., REZNIKOFF W.S.,
GENE 23:149-156(1983).
207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000 FOLD
                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE, 84247342.
MEDLINE,, NGUYEN T.T., BERTRAND K.P.;
POUCLEIC ACIDS RES. 12:4849-4863(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 FOLD
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 PRT;
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                                                                                                                                                                                                                 SEQUENCE OF 1-22 FROM N.A.
 STANDARD;
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 TER2_ECOLI
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               P04483;
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                                                                                                                                                                                                                                                                                                                                                                                                                           PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
PASTEURELLACEAE.
121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                          MIMELH, AOKIT;
MICROBLOL. IMMUNOL. 38:31-38(1994).

**IL FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE ELEMENT: ITS AMINO-TERINAL REGION FORMS A HELIX-TURN-HELLX STRUCTURE. AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE (TETA) PROMOTER OPERATOR SITES.

-!-INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : |||| : |||||| ||| || || | : |
|121 TENGFSLRDGLYAISAVSHFTLGAVLEQOEHTAALTDRPAAPDENLPPLLREALQIMDSD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY SIMILARITY).
3C57D4AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H-T-H MOTIF (POTENTIAL),
INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL. D16172; 6575938; -.
PROSITE: PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
ANTIBIOTIC RESISTANCE; PLASMID.
DNA_BIND 26 H-T-H MOTIF (POFFNET)
                                                                                                                                                                                                                                                                             (REL. 34, CREATED)
(REL. 34, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                              218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 AA.
                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (REL. 34, LAST ANNOTATION UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                                                    181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                               181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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P09164;
01-MAR-1989 (REL. 10, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ||| ||| :| | || ||
181 DGEQAFLHGLESLIRGFEVQL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                   PASTEURELLA PISCICIDA. PLASMID PSP9351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 94328963.
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                                                                                                                                                                                                                                                                             01-OCT-1996
                                                                                                                                                                                                                                                                                                 01-0CT-1996
01-0CT-1996
                                                                                                                                                                                                                                         TER8_PASPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                 TER8_PASPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TER4_ECOLI
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GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 RHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFLC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQYAKEERETPTTDSMPPLLRQAIELFDHQG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |||| : |||:||| ||||| ||| || || :|
121 ENGFSLRDGLYAISAVSHFTLGAVLEQQEHTAALTDRPAAPDENLPPLLREALQIMDSDD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 94204640.
HINRICHS W., KISKER C., DUEVEL C., MUELLER A., TOVAR K., HILLEN W.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. SPECIES-S.ORDONEZ; STRAIN-BM2000; PLASMID-PIP173; MEDLINE; 93204906.
ALLARD J.D., GIBSON M.L., VU L.H., NGUYEN T.T., BERTRAND K.P.; MOL. GEN. GENET. 237:301-305(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVOLVED IN BINDING TO [MG-TC]+.
MAGNESIUM (OF [MG-TC]+ COMPLEX).
830EF8EB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS), AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.8%; Score 678; DB 1; Length 217; 65.0%; Pred. No. 4.4e-56; Live 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB: ZTCT; 03-AER-96.
PROSITE; 20-JUN-96.
PROSITE; PSO1081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING; PLASMID;
ANTIBIOTIC RESISTANCE; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H-T-H MOTIF (POTENTIAL)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS D.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES-E.COLI; STRAIN-J53-1; PLASMID-RA1;
MEDLINE; 85037938.
                                                                                          ESCHERICHIA COLI, AND SALMONELLA ORDONEZ.
                                                                                                                                                                                                                                                                        UNGER B., KLOCK G., HILLEN W.;
NUCLEIC ACIDS RES. 12:7693-7703(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||| ||| :| | |||
181 GEQAFLHGLESLIRGFEVQL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AEPAFLFGLELIICGLEKQL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X01083; G43054; -...
EMBL; X65876; G49075; -...
PIR; S07359; S07359.
PIR; S30287; S30287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                               ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                  PLASMID PIP17
                                                                                                                                          PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INIT_MET
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLASMID PVM111.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSM--PPLLRQAIELFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTIMICROB. AGENTS CHEMOTHER. 37:2699-2705(1993).

-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE ELEMENT: ITS AMINO-TERRINAL REGION FORMS A HELLX-TURN-HELIX STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE (TETA) PROMOTER OPERATOR SITES.
-!- INDUCTION: BY THE (MGT-TETRACYCLINE)+ COMPLEX.
-!- INDUCTION: BY THE (MGT-TETRACYCLINE)+ COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.3%; Score 673; DB 1; Length 207; 64.2%; Pred. No. 1.2e-55; tive 27; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMEL; U00792; G392872; -.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A51DA28B CRC32;
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01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS C.
                                                                                                        01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 AA
                     207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                   ETRACYCLINE REPRESSOR PROTEIN CLASS H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 HQGAEPAFLFGLELIICGLEKQLK 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTIBIOTIC RESISTANCE; PLASMID.
DNA_BIND 26 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (REL. 01, CREATED)
                                                                                01-OCT-1996 (REL. 34, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 AA; 23156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                        STANDARD;
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                                                                                                                                                                                                                                   PASTEURELLA MULTOCIDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=P2862;
MEDLINE; 94153051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                   PASTEURELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986
01-OCT-1996
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                           PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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TER8_PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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PLASMID RP1, AND PLASMID RP4.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 COOGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERE----TPTTDSMPPLLRQAIEL 176
                                                                                                                                                                                                                                                                                                                                                                                                               61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                            MOL. BIOL. EVOL. 2:1-12(1985).

MOL. BIOL. EVOL. 2:1-12(1985).

-:- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE

ELEMENT: ITS AMINO-TERMINAL REGION FORMS A HELIX-TURN-HELIX

STRUCTURE AND BINDS DAR. BINDING OF TETRACYCLINE TO TETR REDUCES

THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                           1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                          (TETA) PROMOTER OPERATOR SITES.
                                                                                                                                                                                                             INVOLVED IN BINDING TO [MG-TC]+ (BY SIMILARITY).
                                                                                                                                                                                                                                           MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                        48.6%; Score 525; DB 1; Length 219; 52.7%; Pred. No. 7.2e-42; tive 32; Mismatches 60; Indels
                                                                                                                                EMBL; M36272; G150946; -.
PIR; A03575; RPECYS.
PROSITE; PS01081; HTH TETR FAMILY; 1.
ATANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING; PLASMID; ANTIBLOTIC RESTANCE.

H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS A (TRANSPOSON 1721).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B., GRECK M., SCHMITT R.;
                                                                                                                                                                                                                                                                      6C9E1828 CRC32;
                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 FDHQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (REL. 01, CREATED)
                                                                                                                                                                                                                                                                      219 AA; 24174 MW;
                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 52.78
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                             100
                                                                                                                                                                                                        45
64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLMEIER H., CRESNAR I
GENE 111:11-20(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. PLASMID-PLASMID RP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSPOSON-TN1721;
MEDLINE; 92192465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESCHERICHIA COLI.
SEQUENCE FROM N.A.
             MEDLINE; 88216101
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                                                                                                                             REGULATORS.
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                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                              Query Match
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TER1_ECOLI
                                                                                                                                                                                                                                               METAL
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TRUEMAN P., SHARPE G.S., BARTH P.T.; SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.

SEQUENCE FROM N.A. TRANSPOSON-TN1721; PLASMID-RP1; MEDLINE; 83299270.

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ENTEROBACTERIACEAE.
WATERS S.H., ROGOWSKY P., GRINSTED J., ALTENBUCHNER J., SCHMITT R.;
NUCLEIC ACIDS RES. 11:6089-6105(1983).
-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT; ITS AMINO-TERRINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOVAR K., ERNST A., HILLEN W.;

MOL. GEN. GENET. 215:76-80(1988).

-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT; ITS AMINO-TERMINAL REGION FORMS A HELIX-TUBN-HELIX
STRUCTURE AND BINDS DAY. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
(TETA) PROMOTER OPERATOR SITES.

-!- SIMILARITY: BELONGS TO THE TETRACARR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                    (TETA) PROMOTER OPERATOR SITES.
-!- INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.7%; Score 515.5; DB 1; Length 216; 52.5%; Pred. No. 5.4e-41; tive 33; Mismatches 60; Indels 3.
                                                                                                                                                                                                                                                                                                                                                             PIR; A03574; RPECRI.
PROSITE; SOSO1081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; TRANSPOSABLE ELEMENT;
DNA-BINDING; ANTIBIOTIC RESISTANCE; PLASMID.
26 45 H-T-H MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TH -> ST (IN REF. 3).
I -> T (IN REF. 3).
DA -> ES (IN REF. 3).
N; F72BDFB1 CRC32;
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01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 AA.
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                                                                                                                                                                                                                                                                        EMBL; X61367; G48198; -
EMBL; X75761; G415985; -
EMBL; X00006; G42509; -
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155
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154
216 AA;
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Matches 106; Conserv
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CONFLICT
SEQUENCE
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DT 01-MAX
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PROKARYOTA; GRACILLICUTES; SCOTOBACTERLA; FACULTATIVELY ANAEROBIC RODS;
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                                                                                                                                                                                                                                                       121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                               1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H-T-H MOTIF (POTENTIAL),
INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                             MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY), MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                            DB 1; Length 211;
                                                                                                                                                                                 Indels
        EMBL; M34933; G155020; ALT_SEQ.
EMBL; X14035; G43056; -
PROSITE: PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
                                                                                                                                                                                99
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TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
ANTIBIOTIC RESISTANCE; PLASMID.
DNA_BIND 26 45 H-T-H MONTH ...-
SITE
                                                                                                                  -> L (IN G43056).
F538C813 CRC32;
                                                                                                                                                        Query Match 47.2%; Score 509.5; DB 1
Best Local Similarity 51.2%; Pred. No. 1.9e-40;
Matches 103; Conservative 29; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              811CB332 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                      210 AA.
                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETRACYCLINE REPRESSOR PROTEIN CLASS G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
                                                  ANTIBIOTIC RESISTANCE; PLASMID.
                                                                                                                 45 V
23585 MW;
                                                                                                                                                                                                                                                                                                                           181 GAEPAFLFGLELIICGLEKQL 201
                                                                                                                                                                                                                                                                                                                                              178 SAEMAFHFGLKSLIFGFSAQL 198
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                                                                                                                45
211 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 93125225.
                                                                                            100
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  REGULATORS.
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                                                                                                                                                                                                                                                                                                                                                                                                  TER7_VIBAN
P51560;
                                                            DNA_BIND
SITE
                                                                                                               CONFLICT
                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CAEGECPKRAVWALRAVSHYVVGSVLEQQASDADERVPDRPDVSEQAPSSFLHVLFHELE 180
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                                                                                                                                           1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WURBHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL.
REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
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Best Local Similarity 28.1%; Pred. No. 2.1e-09;
Matches 61; Conservative 31; Mismatches 88; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, 275555; E250355; -.
PROSITE; PS01081; HTH_TETR_EAMILY; FALSE_NEG.
PROSITE: PS01081; HTH_TETR_EAMILY; FALSE_NEG.
PROTHETICAL PROTEIN; TRANSCRIPTION REGULATION; DNA-BINDING.
BNA_BIND
SEQUENCE 261 AA; 28253 MW; 8CBECC98 CRC32;
/ Match 45.1%; Score 487; DB 1; Length 210; Local Similarity 48.8%; Pred. No. 2.3e-38; nes 98; Conservative 29; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       011023;
01-0CT-1996 (REL. 34, CREATED)
10-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNORATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR CY02B10.17C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 HQGAEPAFLFGLELIICGLEK 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y07H_MYCTU
ID Y07H_MYCTU
               Query Match
                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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210 AA.

PRT;

STANDARD;

MTRR_NEIGO P39897;

a S

RESULT 10 MTRR_NEIGO

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BLATTHER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                           REGULATORS.

EMBL: 225797; 6438189; -.

PIR; 840250; 840250.

PROSITE; PSO1081; HTH_TETR_PAMILY; 1.

TRANSCRIPTION REGULATION; DNA-BINDING; REPRESSOR.

DNA_BIND 32 51 H -7 H MOTIF (POTENTIAL).

DNA_BIND 105 105 H -> Y: IN PENICILLIN-RESISTANT ISOLATES.

SEQUENCE 210 Aa; 24192 MW; F4CABF98 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 CIAQDAADAEGGSWIVF-RHILLHFFERLQSNDIHYKFH-------NILFLKC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIE----LFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 EH--TEQNA--AVIAIA------RKHQAIWREKIT------AVLTEAVENQDLAD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 ----HFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFLC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEISSERIA GONORRHOEAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 27.4%; Pred. No. 0.0021;
Matches 52; Conservative 22; Mismatches 73; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WILSON K.J., JEFFERSON R.A.;
SUBMITTED (OCT-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UID OPERON REPRESSOR (GUS OPERON REPRESSOR).
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                            REGULATORY PROTEIN MTRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
BLATINER F.R., PLUNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 HQGAEPAFLF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 DLDKETAVIF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                     NEISSERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UIDR OR GUSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UIDR_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           059431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UIDR_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
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ECOGENE; EG13435; YCFQ.
PROSITE; PS01081; HTH_TETR_FAMILY; FALSE_NEG.
HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; REPRESSOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 91211614.
REDUCH D.A. CRAM D.S., DIBERARDINO D., LITTLEJOHN T.G.,
SKURRAY R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 86 H-T-H MOTIF (POTENTIAL).
236 AA; 26204 MW; AD1F64FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROKARYOTA; FIRMICUTES; COCCI; MICROCOCCACEAE
                                                                                                                                                                                                    236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 AA.
                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                      154 AKEERETPITDSMPPLLRQAIELFD 178
                                                                                                                           632 KSPELPSPQAEKRPPTLR--LEIID 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (REL. 20, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                       G1787354; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 PTEKQYETLENQLAFLCQQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 RHAMOERTLOO---FLCOR 181
                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAPHYLOCOCCUS AUREUS.
PLASMID PSK1.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-BINDING.
                                                                                                                                                                                               YCFQ_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YP23_STAAU
P23217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA_BIND
                                                                                                                                                                      RESULT 13
                                                                                                                                                                                  YCFQ_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
YP23_STAAU
                                                                                                                                                                                               δy
                                                                          g
                                                                                                     δy
                                                                                                                              g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
KASHIMOTO K., KIM S., KIMURA S., KITACAWA M., KITAKAWA M., MAKINO K.,
MASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
TAGAHI H., TAKEMOTO K., WADA C., YAMAWOTO Y., YANO M.;
SUBMITTED (DEC-1996) TO EMEL/GENBANK/DDBJ DATA BANKS.

-1- FUNCTION: REPRESSOR FOR THE UIDRABC (GUSRABC) OPPERO.

-1- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                             6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                PERIER F., RADEKE C.M., RAAB-GRAHAM K.F., VANDENBERG C.A.; GENE 152:127-163(1995)
-1- IISSUE SPECIFICITY: PRESENT IN A WIDE VARIETY OF TISSUES, IS ABUNDANT IN MOUSE HEART, SKELETAL MUSCLE AND KIDNEY, AND IS MOST ABUNDANT IN TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLG--------VEQPTLYWH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 VKNKRAL--LDALAIEMLDRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHR-----D 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: CONTAINS 4 ANK REPEATS.
-!- SIMILARITY: HIGH, TO OTHER MEMBERS OF THE CLPA/CLPB FAMILY.
EMBL: U09874; G563129; --
MGD; MGI:1100517; SKD3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                            8.8%; Score 95.5; DB 1; Length 196; 25.3%; Pred. No. 0.049; ative 23; Mismatches 32; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.9%; Score 85.5; DB 1; Length 677; 22.4%; Pred, No. 1.8;
                                                                                                                                                                                                                            H-T-H MOTIF (POTENTIAL).
: 6C1840FC CRC32;
                                                                                                                                       EMBL; M14641; G868019; --
EMBL; M14641; G1787904; --
EMBL; D90805; G1742672; --
ECOGENE; EG1267; UIDR.
PROSITE: F991081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; DNA-BINDING; REPRESSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 ATP (POTENTIAL).
76003 MW; FF6EF81E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 1.8; 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-BINDING; REPEAT; ANK REPEAT.
NP_BIND 351 358 ATP
                                                                                                                                                                                                                                    SEQUENCE 196 AA; 21799 MW;
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  66 HFC-PLEGESWODFL 79
                                                                                                                                                                                                                                                                                                                                                                                                  | |:|| :|::
73 RFREPIEGIHFVDYM 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      677 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95137381.
                                                                                                                                  REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKD3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKD3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        060649
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKD3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
g
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ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / MG1655,
BLATINER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
96 GAKVHLGTRPTEKQYE-TLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQE-HQV 153
                                                                     582 GYNVHYGARSIKHEVERRVVNQLAAAYEQDL-----LPGGCTLRITVEDSDKHLL 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 DRDAALDKAMKLFWQHGYEATSLADLVEATGAKAPTLYAEFTNKEGLFRAVLDRYIDRFA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 AKHEAQLFCEEKSVESALADYFAAIANCFTSKDTPAGCFMINNCTTLSPDSGDIANTLKS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 --HHTH-FCPLEG--ESWQDFLRNKAKSF-------RCALLSHRDGAKVHLGTR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN NDH-MFD INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 DKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDR-- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN QACA 5'REGION (ORF 188).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
7.9%; Score 85.5; DB 1; Length 236;
Best Local Similarity 24.5%; Pred. No. 0.52;
Matches 34; Conservative 17; Mismatches 65; Indels 2:
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STRAIN-KL2 / MG1655;
STRAIN-KL2 / GA1655;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X52905; G48717; -.
EMBL, AE000138; G1786505; -.
EMBL, AD7, G1657511; ALT_INIT.
EMBL, 073857; G1657511; ALT_INIT.
PIR, S10899; S10899.
PIR, S1180; S15180.
ECOGENE; EG10111; BETI.
PROSITE; PS01081; HTH TETR.FAMILY; 1.
TRANSCRIPTION REGULATION; DNA-BINDING; REPRESSOR; TRANS-ACTING FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                   66 HFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFLCQQGF 125
                                                                   EMBL; X56628; G46660; -.
PIR; S12393; S12393.
PROSITE; PSO1081; HTH_TETR_FAMILY; 1.
HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; DNA-BINDING; PLASMID;
                                                                                                                                                                                                                                                  43; Indels 30; Gaps
                                                                                                                                                                                                                                                                                   6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

DUNCAN M., ALLEN E., ARAUJO R., APARICIO A.M., CHUNG E., DAVIS K.,

EEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O., LEW H.,

LIN D., NAMATH A., OEFNER P., ROBERED D., SCHRAMM S., DAVIS R.W.;

SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

-i - FUNCTION: REPRESSOR INVOLVED IN CHOLINE REGULATION OF THE BET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- PATHWAY: OSMOREGULATORY CHOLINE-GLYCINE BETAINE PATHWAY.
-i- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL REGULATORS.
MOL. MICROBIOL. 4:2051-2062(1990).
-!- FUNCTION: POSSIBLE TRANSCRIPTIONAL REPRESSOR OF THE QACA GENE.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAMARK I., KAASEN E., ESHOO M.W., FALKENBERG P., MCDOUGALL J., STROM A.R.;
                                                                                                                                                                                                                 Ouery Match 7.8%; Score 84; DB 1; Length 188; Best Local Similarity 22.2%; Pred. No. 0.54; Matches 28; Conservative 25; Mismatches 43; Indels
                                                                                                                                                 24 43 H-T-H MOTIF (POTENTIAL).
188 AA; 22174 MW; D4A58A93 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOL. MICROBIOL. 5:1049-1064(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGULATORY PROTEIN BETI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92065800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                       126 SLENAL 131
                                                     REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 PLONAI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BETI_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12
                                                                                                                                       REPRESSOR.
                                                                                                                                                      DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
BETI_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P17446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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FT DNA_BIND 31 50 H-T-H MOTIF (BY SIMILARITY).

SQ SEQUENCE 195 AA; 21815 MW; BICC26C3 CRC32;

Query Match

Best Local Similarity 27.8%; Pred. No. 0.7;

Matches 20; Conservative 19; Mismatches 25; Indels 8; Gaps 1;

Qy 1 MSRLDKSKVINSALELINEVGIEGLTRKLAQKLGVEQPTLYMHVKNKRALLDA----- 55

Qy 1 MSRLDKSKVINSALELINEVGHDATIAQIARRAGVSTGIISHYFRDKNGLLEATMRDIT 65

Qy 55 --LAIEMLDRHH 64

| | | | | | | | |

Db 66 SQLRDAVLNRLH 77

Search completed: June 9, 1999, 13:01:02
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GenCore version 4.5

Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 1999, 10:28:01; Search time 28:57 Seconds

(without alignments)
399.721 Million cell updates/sec
Title: US-08-486-814-17
Perfect score: 1080
Sequence: 1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207
Scoring table: BLOSUM62
```

180763 seqs, 55169189 residues

sp_invertebrate:*
sp_mammal:*
sp_mhc:*

sp_fungi:* sp_human:*

SPTREMBL_8:*

Searched: Database : sp_organelle:*
sp_phage:*
sp_plant:*
sp_bacteria:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_rodent:*

sp_archea:*

,	Description	Q59466 haemophilus				Q59608 neisseria g	034643 bacillus su										070020 staphylococ		029994 archaeoglob	Q51516 pseudomonas	Q51730 pseudomonas	P96676 bacillus su		m		Q59802 staphylococ		E	Q91290 pleurodeles	018399 drosophila
SUMMARIES	ID	059466	053901	052558	034892	059608	034643	067927	053789	051597	P73186	067157	087854	053295	053310	007001	070020	025951	4 029994	051516	Q51730								2 091290	
	Length DB	!																	Н	205 9								216 9	542 1	405 3
•	Query Match L	57.3	13.8	12.0	11.0	10.2	10.0	4.6		8.8							8.2			8.0			•	7.8	•	٠	7.7		7.7	7.7
	Score	619	149.5	129.5	119	110.5	108.5	101.5	86	. 94.5	94.5	94	94	93.5	92	88	•	7	•	86	85	82	4	84.5		84	ω.		m	83
	Result No.	-	7	e	4	Ŋ	9	7	σ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Q42863 ipomoea bat O67930 aquífex aeo	Q13186 homo sapien O59147 pyrococcus	075181 homo sapien Q54830 streptococc	Q54835 streptococc O08961 rattus norv	O19126 macaca fasc O19127 macaca mula	O60588 homo sapien O14812 homo sapien	O53165 mycobacteri	059306 clostridium	007388 mycobacteri
Q42863 O67930 O06919					060588 014812	053165	059306	007388
თ თ ი	14	0 0	9	4 4	01 00	0	σ	σ
340	2477	847 488	581	285	2442	187	190	82
7.7	7.6	7.5	7.5	7.5	4.4	7.4	7.4	7.4
883	82.5 82.5	81.5	831	80.5	080	80	80	80

ALIGNMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DRHHTHFCPLEGESWQDFLRNNAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
                                                                                                                                                                        N [1]
SEQUENCE FROM N.A.
MEDLINE, 87137315.
A HEUER C., HICKMAN R.K., CURIALE M.S., HILLEN W., LEVY S.B.;
HEUER C., HICKMAN R.K., CURIALE M.S., HILLEN W., LEVY S.B.;
HUGHS C., HICKMAN R.K., CURIALE M.S., HILLEN W., LEVY S.B.;
TO 10-11ke element in Haemophilus parainfluenzae results from a mutation in the repressor gene.";
Though The Tepressor gene.";
The J. BACTERIOL. 169:990-994 (1987).
THE J. BACTERIOL. 169:990-994 (1987).
THE SAL: MISS9; G148989;
THE PROSINE; PROTEIN.
THE TEREFRENEMILY: 1.
THE PROSINEL HETREFRENEMILY: 1.
THE PROSINEL PROTEIN.
THE MISSORAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                              BACTERIA: PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE; HAEMOPHILUS.
                                                                                                                                                                                                                                                                                                                                                                                                                        57.3%; Score 619; DB 9; Length 126; 95.2%; Pred. No. 2.2e-48; tive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                       01-NOY-1996 (TREMBLREL. 01, CREATED)
01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
30S RIBOSOMAL PROTEIN S21.
HAEMOPHILUS PARAINFLUENZA.
                                                                                                                                                                                                                                                                                                                                                                             126 AA; 14541 MW; 107F233B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 08,
ORF1-4 (ACTII).
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.2%
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CQQGF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ANKVF 125
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        053901;
                            Q59466
Q59466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      053901
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Q53901
RESULT
Q59466
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                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S699;
AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., HUTCHINSON C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              117 LAFLCQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEE--------RET 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 MNLLRSGGLHDELAAYGGDLLSTFVTAEALEQSSRNPGTEQGREQAGVFADQLHGYLKSL 202
                                                                                                                                                                                                                                                                                                                       4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDAL----AI 57
                                                                                                                                                                                                                                                                                                                                                    31 LTQDRIVVTALGILDAEGLDALSMRRLAQELKTGHASLYAHVGNRDELLDLVFDIVLTEV 90
                                                                                     MEDLINE; 91347376.
FERNANDEZ-MORENO M.A., CABALLERO J.L., HOPWOOD D.A., MALPARTIDA F.;
FERNANDEZ-MORENO M.A., CABALLERO J.L., HOPWOOD D.A., MALPARTIDA F.;
d'The act cluster contains regulatory and antibiotic export genes,
direct targets for translational control by the bida tRNA gene of
Streptomyces.",
Streptomyces.",
GELL 66:769-780(1991).
FEMBL; M64683; G455360;
PFRM; PF00440; tetR; 1.
SEQUENCE 259 AA; 28268 MW; 16ECA071 CRG32;
                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                                              13.8%; Score 149.5; DB 9; Length 259; 26.0%; Pred. No. 4.5e-06; Live 35; Mismatches 90; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., YU T.W.,
TATLOR M., HOFFMANN D., KIM C.G., ZHANG X., HUTCHINSON C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA; FIRMICUTES; ACTINOBACTERIA; PSEUDONOCARDIACEAE;
                              BACTERIA; FIRMICUTES; ACTINOBACTERIA; STREPTOMYCETES; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIM C.G., YU T.W., FRYHLE C., HANDA S., FLOSS H.G.;
J. BIOL. CHEM. 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 PTTDSMPPLLRQA--IELFDHQGAEPAFLFGLELIICGL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 PAT-SFPNLVHLAGPITSLD---SDRRFELGLEIIIAGL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF040570; G2792330; -.
SEQUENCE 242 AA; 27049 MW; 324EB570 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TREMBLREL. 06, 01-JUN-1998 (TREMBLREL. 06, UL-AUG-1998 (TREMBLREL. 07,
                                                                                                                                                                                                                                                                                           57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMYCOLATOPSIS MEDITERRANEI
              STREPTOMYCES COELICOLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHEM. BIOL. 5:0-0(0002).
                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMYCOLATOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLOSS H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   052558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   052558
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
052558
δλ
                                                                                                                                                                                                                                                                                                                                                     qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
                                                                                                                                                                                                                                                                                                                                                                                                                                              07
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2.
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12.0%; Score 129.5; DB 9; Length 242;

Query Match

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7;
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RA KUNST F., OGASWARA N. MOSZER I., ALBERTINI A.M., ALLONI G.,
RA BURKISS R. BOURSIER L., BRANS A., BRANN M., BRIGNELL S.C., BRON S.,
RA BORRISS R., BOURSIER L., BRANS A., BRANN M., BRIGNELL S.C., BRON S.,
RA BROTILLET S., BRUSCHI C., V., CALDWELL B., CADDANO V., CARTER N.M.,
CHOI S.K., CODANI J.J., CONNETON I.F., CUMMINGS N.J., DANIEL R.A.
RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
RA FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALIZERON N., GHIM S.Y.,
RA GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPPI G.,
RA HOLSAPPEL S., HOSONO S., HULLO, M.F., ITATA M., JONES L., JONES B.,
RA MENANTA D., KASAHRA Y., KLAERR-BLANCHARD M., KLEIN C., KOBAYASHI Y.,
RA COSTTER P., KONINGSTEIN G., KROGH S., KUMANO M., KURITA K., LAVINGSTEIN G., KROGH S., KUMANO M., KURITA K., LAVINGSTEIN G., REDINA N., MELLADO R.P., MIZUNO M.,
RA MAUEL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M.,
RA MOSTIL D., NAKAI S., NOBAK M., NOONE D., O'RELILLY M., CORMA K.,
RA MOSTIL D., NAKAI S., NOBAK M., NOONE D., O'RELILLY M., CORMA R.,
RA PROPORT G., REY M., REYOLD S., RIEGER M., RIVOLTA C., ROCHA E.,
RA ROCHE B., ROSE M., SADAIE Y., SATO T., SCANLAN E., TAKAGI T.,
RA ROCHE B., ROSE M., SADAIE Y., SATO T., SCANLAN E., TAKAGI T.,
RA TAKAHASHI H., TAKEMARU K., TAKEUCHI M., TAMAKOSHI B., TAKAGI T.,
RA TAKAHASHI H., TAKEMARU K., TAKEUCHI M., TAMAKOSHI B., TAKAGI T.,
RA TERPSTRA P., TOGNONI A., TOSALO V., UCHITAMA S., VANDERRO E.,
RA TAKAHASHI H., YATA K., YOSHIDA K., YOSHIRAMA H.E., ZUMSTEIN E.,
RA TOGNIRAMA H., DANCHIN A., TOSALO V., YOSHIRAMA H.E., ZUMSTEIN E.,
RA TOSURIKAMA H., DANCHIN A., TOSALO V., YOSHIRAMA H.E., ZUMSTEIN E.,
RA TOSURIKAMA H., DANCHIN A., TOSALO V., YOSHIRAMA H.E., ZUMSTEIN E.,
RA TOSURIKAMA H., DANCHIN A., TOSALO V., YOSHIRAMA H.E., ZUMSTEIN E.,
RA TOSURIKAMA H., DANCHIN A., TOSALO O, TOSHIRAMA H.E., ZUMSTEIN E.,
RA TOSURIKAMA H., DANCHIN A., TOSALO O, TOSHIRAMA H.E., ZUMSTEIN E.,
RA TOSHIRAMA H., DANCHIN A., TOSALO O, TOSHIRA
                                                                                                                                                   EM----LDRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKV---HLGTRPTEKQY 110
                                                                                                                                                                                   111 ETLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQ----EHQV----AKEERETPTT 163
                                                                                                                                                                                                                                                                 29; Gaps
                                                                                              2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRAL----LDALAI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
      Pred. No. 0.00025;
5; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAPIDUS A., GALLERON N., SOROKIN A., EHRLICH D.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
26.2%; Pred. 115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05,
05,
08,
                             48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTION REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
    Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 98044033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           164 DSM 166
                                                                                                                                                                                                                                                                                                                                                                   196 GSM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             034892
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
034892
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3 RLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                       KARAMATA D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                  034643
                                                                                                                                                                          034643
                                                                                                                             034643
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δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CH95 (MULTIPLY ANTIBIOTIC-RESISTANT STRAIN);
MEDLINE; 9FRATT B.G.;
PAN W., SPRATT B.G.;
"Regulation of the permeability of the gonococcal cell envelope by the mit system."
mL NSYSTEM.".

ML MCROBIOL. 11:769-775(1994).

-:- SIMILARITY: BELONGS TO THE S21P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----HFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTR-PTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 CIAQDAADAEGGSW-----TVFRHTLL------HFFERLOSNDIYYKFHNILFLK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIE---LF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 ILENQLAFICQQGFSLENALYALSAVGHFTLG--CVLEDQEHQVAKE--ERETPTTDSMP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 IVSDQIVCLVTK-LLIENGYASEKTAIHATRGLRSLLHGFTVLIAKEAFEREEDILESLS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION; NEISSERIACEAE; NEISSERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                                           60 LDRHHTHFCPLEGES------WQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYE 111
                                                                                                                                                                                                                                                                                                                 74; Indels 42; Gaps
                                                                                                                                                                                                                                                                                     4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAI----EM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 10.2%; Score 110.5; DB 9; Length 210; Best Local Similarity 27.2%; Pred. No. 0.011; Matches 52; Conservative 21; Mismatches 73; Indels 45.
                                                                                                                                                                                              Query Match 11.0%; Score 119; DB 9; Length 191; Best Local Similarity 23.6%; Pred. No. 0.0016; Matches 48; Conservative 39; Mismatches 74; Indels 4
                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 AA; 24218 MW; E2FEDFC3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ымвь; 225796; G438191; -.
Рискіте; PS01081; HTH_TETR_FAMILY; 1.
PFAM; PF00440; tetR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 PLLRQAIELFDHQGAEPAFLFGL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 FSIR-----TFLSGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30S RIBOSOMAL PROTEIN S21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEISSERIA GONORRHOEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIBOSOMAL PROTEIN
      STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          059608;
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RA MUNDILLE; SUGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
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RA BORLISS R., BOURSETE L., BRANS A., BRAUN M., CARTER N.M.,
RA GUTIS E., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA ENTIAN K.D., ERRINGTON J., FABREI C., FERRARI E., FOULGER D., FERITZ C.,
RA ETUITA M., FUJITA Y., FUNA S., GALIZZI A., GRAILERON N., GHIM S.Y.,
RA GUSER P., GOFFEND A., GOLIGHTLY E.J., GRANDI G., GUISEPIE G.,
RA GUTER P., KOSONO S., HAREN-BLANCHARD M., KLEIN C., KOBAPSKII Y.,
RA KORAMATA D., KASAHRAA Y., KRORH S., KUMANO M., KURITA K., LAPIDUS A.,
RA KARAMATA D., KASAHRAA Y., LAZAREVIC V., LEE S.M., LEVINE A., LIUD H.,
MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M.,
RA MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., RELLADO R.P., MIZUNO M.,
RA MOSCHI D., NAKAI S., NOBACK M., NOONE D., O'REILLY M., OOGTWELLE B.,
RACHER B., ROSE M., SADAIE Y., SAND T., SERNORSKA A., SERROR S.J.,
RA RACHOPORT G., REY M., REYNOLLS S., RIEGER M., RIVOLTA C., ROCHA E.,
RACHARSHI H., TAKEMARU K., TAKEGURI M., TAKANORI B., TAKANOR T.,
RACHARSHI H., TAKEMARU K., TAKEGURI M., TAKANORI R., WANDURDER E., WEDLER H.,
RACHARSHI H., TAKEMARU K., TAKEGURI M., TAKANORI R., WANDURD R., WENTER R., WANDURD R., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE; BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. LAZAREVIC V., SOLDO B., RIVOLTA C., REYNOLDS S., MAUEL C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=168;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF0112113; G2618838; -.
EMBL; Z99122; E1184426; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TREMBLREL. 05,
01-JAN-1998 (TREMBLREL. 05,
01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.0%
Best Local Similarity 19.6%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00440; tetR;
178 DHQGAEPAFLF 188
                                                                                     155 DDLDKETAVIF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 96181548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAM REPRESSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSEUDOMONAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLASMID CAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLE S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=PPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                051597;
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                        ACCOOR NOT THE READ TO THE READ TO THE READ TO THE READ TO THE READ THE REA
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                                                                                                                                              123 QGFSLENALYALSAVGHFTLGCVLEDQEHQ-------VAKEERETPTTDSM 166
                                                                                                                                                                                      62 RGSILEQTEGDLYKDLL-------83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-VF5;
MEDLINE; 98196666.

MEDLINE; 98106666.

GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;

"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., FELLERDAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V., EMBL, AE000776; G2984362, -...
PROSITE; PSO1081; HTH_TETR_FAMILY; 1
SEQUENCE 192 AA: 22259 WW: D2E83A94 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 RHHTHFCPLEGESWQDFLR-----NKAKSFRCALLSHRDGAKVHLGTRPTEKQY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 RHKLEVALQRGETDEBILLESIVDTLIDYAFSNPESFRFLNLXH------LLKEY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 ETLENQ-----LAFICQOGFSLENALY---ALSAVGHFTLGCVLEDQEHQVAKEER---- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GEVKNLPGELILKFL-----NGLYLKRKLKTYPEIALAVVTGSVERVFIFKERNFLD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Indels 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNK----RALLDALAIEMLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
9.4%; Score 101.5; DB 9; Length 192;
Best Local Similarity 22.7%; Pred. No. 0.06;
Matches 45; Conservative 34; Mismatches 68; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-505-1998 (TREMBLREL. 07, CREATED)
01-505-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL REGULATOR (TETR/ACRR FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
                                                                                                                                                                                                                                                                                                                                                                                            192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 AA.
                                                                                                                                                                                                                                167 PPLLRQAIELFDHQG-----AEPAFLF 188
                                                                                                                                                                                                                                                                      120 KOLLVDYLKTMGEKGVIQTGNEAEHADVF 148
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 -- ETPTIDSMPPLLRQAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 YDEETIKKELKKVLKSAI 190
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQUIFEX AEOLICUS
                                                                                                                                                                                          83 ----
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053789
ID 053789
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BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE;
MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 RHHTHFCPL-EGESWQDFLRNKAKSFRCALLSHRDG-----AKVHLGTRPTEKQYET--- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 DIIIMLNRVGAGRARDDAVLVWAGAYR-SYAHHHPGRYSAFTRMPLGGDDPEYTAATRGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "camR, a negative regulator locus of the cytochrome P-450cam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 86223770.
KOGA H., ARAMAKI H., YAMAGUCHI E., TAKEUCHI K., HORIUCHI T.,
GUNSALUS I.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
9.1%; Score 98; DB 9; Length 196;
Best Local Similarity 27.3%; Pred. No. 0.13;
Matches 42; Conservative 24; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.; SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                     HAMLIN N., CHURCHER C.M.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PUTATIVE TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL; AL021943; E1253107; -.
SEQUENCE 196 AA; 21262 MW; 17D86001 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 LENQLAFLCQQGFSLENALYAL----SAVGHFTL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AAPVIAVLSSYGLDGEQAFYAALEFWSALHGFVL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hydroxylase operon.";
J. BACTERIOL, 166:1089-1095(1986).
                                                                                                                                                       MYCOBACTERIUM TUBERCULOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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97 DLLCSEKFRNIYFEKIEDAKRRFEKFLEKHFPSKAEILSEIILGFLRQLILHYVIKEERE 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 --LCQQGF----SLENALYAL-----SAVGHFTLGCVLEDQEHQVAKEERE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KERILEVSKELFFEKGYQGTSVEEIVKRANLSKGAFYFHFKSKEELI----TEIIERTHK 59
                                                                                                              68 CPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEK-QYETLENQLAFLCQQGFS 126
                                                                                                                                                               96 ----AGWVEILTD-----RRMFH 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                      46 RILKGALKLFGTKGYEGTTTKDLAQAANVAEGTLFRYFTNKKAILVEVAT----- 95
     8 KVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHTHF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 KIISL-----FEENKEKTPEELL-------EMFLEVLYREKKVVYIFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=VF5;

BECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
EMBL, ABOO0721; G298349; -.
SEQUENCE 179 AA: 21554 MW; E359173B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.7%; Score 94; DB 9; Length 179; Best Local Similarity 21.4%; Pred. No. 0.26; Matches 47; Conservative 33; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL REGULATOR (TETR/ACRR FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : | |::| |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                      127 LENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSM 166
                                                                                                                                                                                                                                                  BĀCTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX
                                                                                                                                                                                                                                                                                                                                                                                                            179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQ
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 392:353-358(1998)
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98196666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQUIFEX AEOLICUS
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                                                                                                                                                                                                                                                                                                                                                                                                            067157
                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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ID 06
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KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYALIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
TABATA S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                     ARAWAKI H., SAGARA Y., TAKEUCHI K., KOGA H., HORIUCHI T.; "Nucleotide sequence of the gene encoding a repressor for the cytochrome P-450cam hydroxylase operon on the Pseudomonas putida CAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKN----KRALLDALAIEMLD 61
                                                                    MEDLINE; 93326643.
ARAMARI H., KOGA H., SAGARA Y., HOSOI M., HORIUCHI T.;
"Complete nucleotide sequence of the 5-exo-hydroxycamphor
dehydrogenase gene on the CAM plasmid of Pseudomonas putida (ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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8.8%; Score 94.5; DB 9; Length 236;
Best Local Similarity 22.5%; Pred. No. 0.33;
Matches 36; Conservative 24; Mismatches 55; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TABATA S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 26.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.8%; Score 94.5; DB 9; 28.6%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 AA; 26384 MW; A8D84E37 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 AA; 20438 MW; 56E43196 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Mismatches
                                                                                                                                                                                                         BIOCHIM. BIOPHYS. ACTA 1174:91-94(1993).
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PROSITE; PS01081; HTH_TETR_FAMILY; 1.
PFAM; PF00440; LELR; 1.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TREMBLREL. 02, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNECHOCYSTIS SP. (STRAIN PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 RHH---THFCPLEG--ESWQDFLR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 AYHGGTEERGPLKGIRDGWATFLQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.8%
Best Local Similarity 28.6%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOCHIMIE 76:63-70(1994).
EMBL; D14680; G473745; -.
PFAM; PF00440; tetR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                    STRAIN-PPG1
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MEDLINE; 97000351.
REDEMBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
KIRASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MOI. MICROBIOL. 21:77-96(1996).
EMBL, ALO31013: E1309426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
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BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
8.7%; Score 94; DB 9; Length 217;
Best Local Similarity 34.1%; Pred. No. 0.33;
Matches 29; Conservative 14; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BARRELL B.G., RAJANDREAM M.A., PARKHILL J., COLE S.T., SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                         STREPTOMYCES COELICOLOR.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; STREPTOMYCETES; STREPTOMYCES.
                                                                                                                                                                                                                                                                                              SEGER K.J., HARRIS D.;
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PUTATIVE TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MTYOOTEST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 HHTHFCPLEGESWQDFLRNKAKSFR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                  STRAIN=A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                              66 HFCP---LEGESWQDFLRNKAKSF--------RCALLSHRDGAKVHLGTRP 105
                                                                                                                                                                                                                                                                                                                                                                                                                            -----SAVGHF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 TLAMAEMFNNELREMELNRAALELAAFAAFGSAASATEWWLGPEPDSPRRMPREQFVAHL 210
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MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE; MYCOBACTERIAD.
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                      6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                            32 RNEIVDAAFRAIDRIGPE-LSVRQIABEAGTAKPKIYRHFTDKSDLLEAIGMRLRDMIWA 90
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BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                             51;
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                                                                                                                                                                                 Query Match 8.7%; Score 93.5; DB 9; Length 246; Best Local Similarity 19.0%; Pred. No. 0.42; Matches 41; Conservative 42; Mismatches 82; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.5%; Score 92; DB 9; Length 213; Best Local Similarity 35.8%; Pred. No. 0.48; Matches 24; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLIVER K., HARRIS D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TREMBLREL. 06, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
leprae.";
PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL; AL021287; E1237796; -.
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EMBL; AL021646; E1248751; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 TEKQYETLENQLAFLCQQGFSLENALYAL-------
                                                                                                       246 AA; 27618 MW; DC3E2076 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 TIIMMGVIVGTAEALGIAVDPOQPIHDAVPNNPAVR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 T---LGCVLEDQEHQVAKEERETPTTDSMP--PLLR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 AA; 23120 MW; 2316B357 CRC32;
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                                                                                 HYPOTHETICAL PROTEIN.
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RA AZEVEDO V. BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BOURSIES R., BOURSTER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
BORISISS R., BOURSTER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA BROUILLET S., BUTSCHE L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA CHOI S.K., CODAUI J.J., CONNERTON I.F., CUMMINOS N.J., DANIEL R.A.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRAIR E., FOULGER D., FRITZ C.,
RA GINERR P., GOFFEAN A., GOLIGHTUX E.J., GRANDI G., GUISEPPI G.,
RA HOLSAPPEL S., HAGA K., HALECH J., HARMOT A., HILBERT H.,
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RA GINERR P., KONINGSTEIN G., KROGH S., KUMIN M., KLEIN C., KOBAYSHI Y.,
RA MOESTL D., NARAHARA Y., LAZARENTU V., LEE S. M., LEVINE A., LIUL M.,
RA MOESTL D., NARAI S., NOBACK M., NOONE D., O'RELLLY M., OGAWA K.,
RA RAPOPORT G., REY M., REYNOLDS S., RIGGER W., SHELLEN B., PORTRELLE B.,
RAPOPORT G., REY M., REYNOLDS S., RIGGER W., SHONE C., PORTRELLE B.,
RARABSHI H., TAKEMARU K., TAKEUCHI M., TAKONIN C., TAKONI C.,
RA SERROR P., SHIN B.S., SOLIDO B., SORNIN A., TAMAKA T.,
RANDENGER R., SOCFFONE F., SERIGUCHI M., TAMAROSHI A., TAMAKA T.,
RANDENGER R., SOCFFONE F., SERIGUCHI M., TAMAKOSHI A., TAMAKA T.,
RANDENGER R., SADALE Y., SALDIE Y., SANDANE S., VANDENBOL M.,
RANDENGER R., SOLIO B., SORNIN A., TAMAROSHI A., TAMAKA T.,
RANDENGER R., VANDENGER P., WARBUTT R., WEDLER E., WEDLER H.,
RANDENGER R., VANDENGER P., WARBUTT R., WEDLER E., WEDLER H.,
RANDENGER R., VANDENGE P., WIRTER P., WARBUTT R., WEDLER E.,
RANDENGER R., YOSHIKAWA H., PANDENGE R.,
RANDENGE R., WARBUT R., YOSHIKAWA H., PANDELLE R.,
RANDELLE R., ROSE W., SADALE Y., VOSHIKAWA H., PANDELLE R.,
RANDER R., WOSHIKAWA H., DANCHIN R., TAMAMANIT R., WASHIKAWA H., DANCHIN R., TAMAMANIT R.,
RANDER R., WOSHIKAWA H., DANCHIN R., TAMAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The complete genome sequence of the gram-positive bacterium Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                  01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 22.2 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBNITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 294043; E313126; -.
EMBL; 299121; E1186136; -
EMPL; PF00440; tetr; 1
HYPOTHETICAL PROTEIN.
SEQUENCE 194 AA; 22227 MW; D3457AEC CRC32;
                                                                                                                                                                        194 AA.
                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        BACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 98044033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEOUENCE FROM N.A.
  65 THFCPLE 71
                                           69 ----PLE 71
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                                                                                                                                                                                                                                                                                                                                                                    BACILLUS.
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                                                                                                            RESULT 15
007001
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Gaps

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Query Match
8.2%; Score 89; DB 9; Length 194;
Best Local Similarity 31.0%; Pred. No. 0.8;
Matches 18; Conservative 17; Mismatches 21; Indels

Search completed: June 9, 1999, 13:00:33 Job time: 9152 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM protein - protein search, using sw model

June 9, 1999, 12:59:17; Search time 23.43 Seconds (without alignments) 178.687 Million cell updates/sec Run on:

US-08-486-814-19 1080 1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207

Perfect score: Sequence: Title:

BLOSUM62 Scoring table: 162890 seqs, 20225328 residues Searched:

A_Geneseq_34:* Database : pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		ced In-10 d	ed In-10 der	ed reverse T	der let reb	9 :	FIOCETII CICCOCC DY	tuno ma-10	d-type E coli	ti-chimeric tr	ti-chimeric t	Protein encoded by	se of	sact	S	ASK75 op	규	leckstrin	ansa	TAk er	tated Tet	etra	ET TO	Tet repre	d Tet repre	Tet repre	Tet repre	Tet repre	Tet	g	Tet	Tet repre	Tet repre	Tet repre	Tet r	Tet repre	d Tet	Tet repre	Tet repre	ed Tet repre	ed Tet	t repre	r repre
SUMMARIES	9		R8	R 83	W08	20	3	3	Rep	0 6	2 3	7.7	W.7	R4	R64	88	R8	W2	WS	R8	Ö,	WO	W	8	8	8	M 0	MO	M M	8	8	3	8	8	8	8	8	M _O	8	8	×	3	MO	M
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	Length	3	33														•																											
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οy qq RESULT 2 R89764 11D R89764 standard; Protein; 207 AA. AC. R89764;

RESULT 1 R89761 DT R89761	33 95.6 207 1 W08307 Mutated Tet repres 32 95.6 207 1 W08309 Mutated Tet repres	ALIGNMENTS	andard; Protein; 335 AA. 96 (first entry) 10 derived Tet repressor/HSV fusion protein. 110 derived Tet repressor/HSV virion protein 16 110 otein; gene expression; regulation; inhibition; ac 1110. 1110. 1110. 110. 110. 110. 110. 110. 110. 110. 110. 110. 110. 110. 110. 110. 1	Query Match Best Local Similarity 100.0%; Pred. No. 6.8e-115; Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEOPTLYWHYKNKRALLDALAIEML 60
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	95		andar 196 (18-10. 195. U 195. U	Simi 7;	CLDKSK CLDKSK HTHFC
444 130 No. 20 N	1033		1 39761 st 2-JUL-15 2-JUL-15 2-JUL-15 2-JUL-16 Ranscorf Ranscorf Ranscorf Ranscorf Ranscorf Ranscorf Ranscorf Ranscorf Ranscorf Ranscorf PUL-16 1-JUL-16 5-JUL-16 1-JUL-17 1-JUL-16 5-JUL-16 1-JUL-16 5-JUL-16 5-JUL-16 6-JUL	ry Match Local	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tet; tetracycline; Tc; operator; transcription; regulation; inducible; repressor; gene expression; therapy; transgenic animal; disease model.
 07-JUL-1996 (first entry)
Mutated Tn-10 derived Tet repressor.
Tet repressor: Herpes simplex virus; HSV; virion protein 16; VP16; fusion protein; gene expression; regulation; inhibition; activation;
                                                                                                                                                                                                                                                                                                        Claim 44: Page 80: 112pp; English.

Fusion proteins comprising a first polypeptide which binds to a tet operator sequence in the presence of tetracycline or a tetracycline analogue, operatively linked to a second polypeptide which either activates or inhibit transcription in eukaryotic cells may be used to activate or inhibit transcription. Such proteins may be used to gene therapy and for expression of gene products in transgenic organisms. Induction of gene expression is rapid, efficient and strong, typically 1000-2000 fold. The inducing agent does not cause strong, typically 1000-2000 fold. The inducing agent does not cause sequence is a mutated In-10 tet repressor used in a transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DRHHTHECPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New tetracycline-regulated transcription modulators - comprising fusion proteins which bind to tet operator sequences to activate or inhibit transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 207;
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/note= "Lys replaces wild-type Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAR-1997 (first entry)
Mutated reverse Tet repressor/VP16 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1080; DB 1; 100.0%; Pred. No. 3.4e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W08293 standard; Protein; 335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibiting fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207; Conservative
                                                                                                                    29-JUN-1995; U08179.
01-JUL-1994; US-270637.
15-JUL-1994; US-275876.
                                                                                                                                                                03-FEB-1995; US-383754
07-JUN-1995; US-486814.
                                                                                                                                                                                                                         Bujard H, Gossen M;
WPI; 96-087666/09.
N-PSDB; T11352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                            Transposon In-10.
                                                                                                                                                                                            (BUJA/) BUJARD H.
                                                                                                                                                                                                          (GOSS/) GOSSEN M
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                                                            transcription.
                                                                                     WO9601313-A1.
                                                                                                        18-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
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Well's y-102JUS/US.

Whicheld acid encoding tetracycline-inducible transcription
regulatory fusion protein - comprising modified tetracycline
regulatory fusion protein - comprising modified tetracycline
regulatory fusion protein - comprising modified tetracycline
regulator, useful for modulating eukaryotic gene expression
Example 1: Page 77-78: 117Pp; Engalish.
W08293 represents a "reverse" Tet repressor (TTER), i.e. a wild-type
control mutated so as to bind its target in the presence
rather than the absence of tetracycline (TC), fused to a C-terminal
controlled of VP16 (herpes simplex virus virion protein 16), a
transcriptional activator. The fusion protein forms a Tc-controlled
controlled of VP16 (herpes simplex virus virion protein 16), a
transcriptional activator (TTA). The main invention of the
controlled propertied TetR proteins that bind to modified
controlled propertied TetR proteins can be fused to any transcription
controlled by altering the condrol transcription of a tetO-4C
controlled by altering the condrol transcription of the protein can be
controlled by altering the condrol. Of tetracycline (or an analogue) in
controlled by altering the condrol. Of tetracycline (or an analogue) in
controlled by altering the condrol. Of tetracycline (or an analogue) in
controlled by altering the condrol. Of tetracycline (or an analogue) in
condels for the study of disease and also for the study of gene
condels for the study of disease and also for the study of gene
condens of inducer are not required. The Tc-inducible system allows
concurs. Of inducer are not required.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                            "C-terminal fragment of VP16 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 100.0%; Score 1080; DB 1; Length 335; Similarity 100.0%; Pred. No. 6.8e-115, 77; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                Gossen M, Helbl V, Hillen W, Schnappinger D;
                                                                                                                                                              /note= "Asp replaces wild-type Gly" 208. .335
                                           'note= "Asn replaces wild-type Asp"
                                                                                                        'note= "Ser replaces wild-type Leu"
                                                                                  /label- substitution
                          /label- substitution
                                                                                                                                               /label= substitution
                                                                                                                                                                                         .335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207; Conservative
                                                                                                                                                                                                                                                                                             US-485971.
                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                       06-JUN-1996; U09049
                                                                                                                         misc_difference 102
                                                            misc_difference 101
    misc_difference 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 AA;
                                                                                                                                                                                                                                                                                                                                               97-052305/05
                                                                                                                                                                                                                                                                                  07-JUN-1995; US-
(BADI ) BASF AG.
                                                                                                                                                                                                                         WO9640892-A1.
                                                                                                                                                                                                                                                      19-DEC-1996
                                                                                                                                                                                                                                                                                                                                  Bujard H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                      domain
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121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180

W08297 standard; Protein; 207 AA.

RESULT

AC PA

19-MAR-1997 (first entry)

W71323

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w08297 represents a mutated Tet repressor (TetR). This sequence was used to create a fusion protein, comprising the mutated TetR fused to a verbA silencer domain (see T45728, W08299). The fusion protein forms a Ter-controlled transcriptional activator (TPA). The main invention of the specification concerns modified TetR proteins that bind to modified class B tet operator sequences tetO-4c and tetO-6c (see T45711 and requists B tet operator sequences can be tused to any transcription or regulatory polypeptide and used to control transcription of a tetO-4c or tetO-6c linked gene. Nucleic acid encoding such a fusion protein or tetO-6c Inked gene. Nucleic acid encoding such a fusion protein can be introduced into a cell and transcription of the protein can be controlled by altering the concn. of tetracycline (or an analogue) in the cell, as appropriate. This ability to modulate gene expression in the cell, as appropriate. This ability to modulate gene expression in protein prode in cultured cells or transgenic animals. The control of the protein prode in cultured cells or transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tc-inducible system is also useful for the prodn. of transgenic animal models for the study of disease and also for the study of gene function e.g. during differentiation. The Tc-inducible system allows rapid activation of gene transcription without cellular toxicity, high concns. of inducer are not required.
Mutated Tet repressor.
Tet; tetracycline; Tc; operator; transcription; regulation; inducible;
repressor; gene expression; therapy; transgenic animal; disease model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI: 97-052305/05.
WPI: 97-052305/05.
Nucleic acid encoding tetracycline-inducible transcription
regulatory fusion protein - comprising modified tetracycline
repressor able to bind mutant tet operator, fused to transcription
regulator, useful for modulating enkaryotic gene expression
Example 5; Page 86-87; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gossen M, Helbl V, Hillen W, Schnappinger D;
                                                                                                                                                                                                                                                                                                                                                   /label= substitution
/note= "Asp replaces wild-type Gly"
                                                                                                                                                                                                                                                                                                       'note= "Ser replaces wild-type Leu"
                                                                                                                                                            'note= "Lys replaces wild-type Glu'
                                                                                                                                                                                                                                'note= "Asn replaces wild-type Asp'
                                                                                                                                                                                                               /label= substitution
                                                                                                                                                                                                                                                                                 /label= substitution
                                                                                                                                        /label- substitution
                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995; US-485971.
(BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-1996.
06-JUN-1996; U09049.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                           misc_difference 102
                                                                                                                                                                                                                                                         misc_difference 101
                                                                                                                                                                                    misc_difference 95
                                                                                                                  misc_difference 7
                                                                                                                                                                                                                                                                                                                                                                                                  WO9640892-A1
                                                                         Synthetic.
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61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                121 COOGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                        61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                   181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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RESULT

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Example 1; Columns 67-68; 63pp; English.

The present sequence is encoded by a "reverse" Tet repressor (rTetR), which binds to its target DNA in the presence rather than the absence of tetracycline. The sequence was generated by chemical mutagenesis.

TetR is used in the course of the invention. The specification describes a method for regulating expression of a Tet (tetracycline) operator-linked gene in a cell of a subject. The method comprises introducing into the cell a nucleic acid encoding a fusion protein which inhibits transcription in eukaryotic cells, the fusion protein comprising a polypeptide which binds to a Tet operator sequence, comprising a polypeptide which binds to a Tet operator sequence.

Transcription in enkaryotic cells and modulating the concentration of terracycline (analogue) in the subject. The method is used for the regulation of gene expression system, using tetracycline (analogues).

The system enables a gene coupled to the system to be induced in the Sequence of Tet and then stopped when Tet is removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Tetracycline based regulation of gene expression - uses a tetracycline operator sequence joined to a gene of interest, the gene of interest being induced in the presence, but not absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1080; DB 1; Length 335; 100.0%; Pred. No. 6.8e-115; tive 0; Mismatches 0; Indels 0;
                               04-DBC-1998 (first entry)
Protein encoded by "reverse" Tet repressor sequence.
Tet repressor; rTetR; tetracycline; regulation; expression;
Tet operator-linked gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-1998 (first entry)
Protein encoded by mutant Tn10-derived tet repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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W71327;
W71323 standard; Protein; 335 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 207; Conservative
                                                                                                                                                                 07-JUN 1995, 485978.

07-JUN 1995, US-485978.

14-JUN 1993, US-076726.

14-JUN 1993, US-076726.

14-JUN 1994, US-266452.

01-JUL 1994, US-276876.

15-JUL 1994, US-275876.

(BADI ) BASE AG.

(KNOL ) KNOLL AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           Bujard H, Gossen M;
WPI; 98-541795/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; V60076
                                                                                                               Synthetic.
US5814618-A.
29-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression system, using tetracycline (analogues). The system enables a gene coupled to the system to be induced in the presence of Sequence 207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tTA; transactivator; tetracycline-controllable transactivator; conditional inactivation; homologous recombination; gene expression; gene regulation; gene therapy; tetracycline-resistance; tetR; transgenic animal.
                                                                                                                                                                                                                                                                                                                           Tetracycline based regulation of gene expression - uses a tetracycline operator sequence joined to a gene of interest, the gene of interest being induced in the presence, but not absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1080; DB 1; Length 207; 100.0%; Pred. No. 3.4e-115; Live 0; Mismatches 0; Indels 0;
 repressor; tetracycline; regulation; expression; operator-linked gene; tet operator.
                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Columns 81-82; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAEPAFLFGLELIICGLEKQLKCESGS 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-1995 (first entry)
tTA transactivator.
                                                                                                                                          14-JUN-1993; US-076726.
14-JUN-1994; US-260452.
01-JUL-1994; US-270637.
15-JUL-1994; US-275876.
06-FEB-1995; US-383754.
(RADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 207; Conservative
                                   Synthetic.
US5814618-A.
29-SEP-1998.
07-JUN-1995; US-485978.
14-JUN-1993; US-076327.
                                                                                                                                                                                                                                                                          Gossen M;
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61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regulatory systems using tetracycline-controllable transactivator (tTA) - useful for conditional inactivation or modulation of gene expression in a host cell or animal Disclosure; Page 46-48; 103pp; English.
A 397 bp Mlul/FokI fragment of pMSvP16 coding for the C-terminal 130 amino acids of VP16 of HSV was blunted and inserted in pHB14-1. The resulting plasmid, pHB15-1, encoded a tetR-VP16 fusion protein, or tetracycline-controllable transactivator (TTA), whose sequence is given in Q76264, and the encoded protein sequence in R64808.
                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1996 (first entry)
Wild type In-10 derived Tet repressor.
Tet repressor: Herpes simplex Virus; HSV; virion protein 16; VP16;
fusion protein; gene expression: regulation; inhibition; activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion proced as comprising a first polypeptide which binds to a tet operator sequence in the presence of tetracycline or a tetracycline analogue, operatively linked to a second polypeptide which either activates or inhibits transcription in eukaryotic cells may be used to activate or inhibit transcription. Such proteins may be used to activate or inhibit transcription. Such proteins may be used to regulate gene expression in cells and may be particularly useful for gene therapy and for expression of gene products in transgenic organisms. Induction of gene expression is rapid, efficient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tetracycline-regulated transcription modulators - comprising fusion proteins which bind to tet operator sequences to activate or
                                                                                                                                                                                                                                                                                                                                                Length 335;
                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                      98.0%; Score 1058; DB 1;
98.1%; Pred. No. 2.2e-112;
tive 2; Mismatches 2;
                                                         Gossen M, Salfeld JG, Voss JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-1995; U08179.
01-JUL-1994; US-270637.
15-JUL-1994; US-275876.
03-FEB-1995; US-383754.
07-JUN-1995; US-486814.
14-JUN-1994; U06734.
14-JUN-1993; US-076327.
(BADI ) BASF AG.
Bujard H, Gossen M, Sc
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                                                                                                                                                                                                                                                                                   335 AA:
                                                                        WPI; 95-036472/05.
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N-PSDB; T11351.
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WO9601313-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BUJA/) BUJARD H. (GOSS/) GOSSEN M.
                                                                                            N-PSDB; Q76264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-1996.
                                                                                                                                                                                                                                                                                   Sequence
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regulatory fusion protein - compension modified tetracycline respectsor able to bind mutant tet operator, fused to transcription regulator, fusion protein - compension modified tetracycline repressor able to bind mutant tet operator, fused to transcription regulator, useful for modulating eukaryotic gene expression regulator, useful for modulating eukaryotic gene expression (Tansposon IO (Thil) of E. coli. The wild-type sequence is used for the production of a mutated TetR (so as to bind its target in the presence rather than the absence of tetracycline). Mutant TetR proteins the production of a mutated TetR (so as to bind its target in the presence rather than the absence of tetracycline). Mutant TetR proteins can be fused to a transcription of the specification concerns modified TetR proteins that bind to modified class B tet operator activator (tTA). The main invention of the specification concerns modified TetR proteins that bind to modified class B tet operator proteins can be fused to any transcription regulatory polypeptide and used to control transcription of a tetO-4C or tetO-6C linked gene.

Nucleic acid encoding such a fusion protein may be introduced into a cell and transcription of the protein can be controlled by altering the concor. Of tetracycline (or an analogue) in the cell, as appropriate. This ability to modulate gene expression in a predictable way is very useful in gene therapy and for recombinant protein produ. In cultured cells or transgenic animal models for the study of disease and also for the study of gene function e.g. during differentiation. The Teinducible system allows rapid activation of gene transcription e.g. during deflerentiation.

Tetal control transgenic animal models for the study of disease and also define teals.

Tetal control teals allows rapid activation of gene transcription e.g. during deflerentiation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wild-type E.coli Tn10-derived Tet repressor.
Tet; tetracycline; Tc; operator; transcription; regulation; inducible; repressor; gene expression; therapy; transgenic animal; disease model;
                                                                                                                                                                                                                                                                                                                                                                           61 DRHHTHFCPLEGESWQDFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                                               61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                          1 MSRLDKSKVINSALELLNEVGIEGLFTRKLAQKLGVEQPFLYWHVKNKRALLDALAIEML 60
strong, typically 1000-2000 fold. The inducing agent does not cause pleitropic effects or cytotoxicity in eukaryotic cells. This sequence is the wild type In-10 tet repressor.
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0
                                                                                                                                                Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bujard H, Gossen M, Helbl V, Hillen W, Schnappinger D; WPI; 97-052305/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding tetracycline-inducible transcription
                                                                                                                                                                                                   Indels
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                                                                                                                                                Score 1058; DB 1;
Pred. No. 1.1e-112;
                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W08296 standard; Protein; 207 AA.
                                                                                                                                              98.0%;
98.1%;
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07-JUN-1995; US-485971.
(BADI ) BASF AG.
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                                                                                                                                                                          Similarity
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WO9640892-Al.
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                                                                                                                                                   Query Match
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and envelope protein

Sisclosure; Fig 4A-C; 84pp; English.

This fusion protein comprises a multi-chimeric transactivator, designated rTAER, that is composed of (from the N-terminus to the transcriptional activation domain of herpes simplex virus VD16, and transcriptional activation domain of herpes simplex virus VD16, and the ligand binding domain of the oestrogen receptor. An inducible expression system of the invention is composed of tTAER and a minmal promoter (see V1775) derived from the immediate early gene of cytomegalovirus linked to 7 tandem copies of the tet operator (tetO) that is the binding site for tetR, which in turn can be of cytomegalovirus linked to 7 tandem copies of the tet operator (tetO) that is the binding site for tetR, which in turn can be of cytomegalovirus linked to 7 tandem copies of the tet operator (tetO) that is the binding site for tetR, which in turn can be converted to a nuclectide sequence of interest. The invention relates to packaging cell lines derived from HeLa, DI7, MDCK, BHK or preferably Cf2Th cells and recombinant retroviral particles.

Froduced by them, particularly pseudotyped retroviral particles.

Froduced by them, particularly pseudotyped retroviral particles.

Froduced by them inducible expression system. The products can be used for the inducible expression in cells of polypeptides, e.g. cytotoxic products or therapeutic agents. The activation of the inducible expression system requires 2 independent signals, thus central particular particular particular agents. The activation.
                                                                                                                                                                                                                    61 DRHHTHFCPLEGESWODFLRNKAKSFRCALLSHRDGAKVHLGTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                           DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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                                                 Gaps
                                                                                            1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                       1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multi-chimeric transactivating factor rTAER fusion protein. Multi-chimeric transactivating factor; rTAER; tetR; tetracycline repressor; HSV; oestrogen receptor; promoter; packaging cell line; retrovirus; retroviral particle; vector; gene delivery; gene therapy.
Length 207;
                                               Indels
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06-AUG-1997; UJ3846.
07-AUG-1996; US-694652.
(CITY ) CITY OF HOPE.
(REGC ) UNIV CALIFORNIA.
Chen S, Friedmann T, Miyanohara A, Prussak CE, Yee J;
N-PSDB; V17756.
  Score 1058; DB 1;
Pred. No. 1.1e-112;
                        Pred. No. 1.16
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                                                                                                                                            181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Herpes simplex virus.
Chimeric - Mammalia.
WO9805759-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W48357 standard; Protein; 651 AA
  98.0%;
98.1%;
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Query Match
Best Local Similarity 98.1
Matches 203; Conservative
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Sequence 65
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Gaps

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98.0%; Score 1058; DB 1; Length 651; 98.1%; Pred. No. 5.6e-112; ive 2; Mismatches 2; Indels (

Query Match 98.0° Best Local Similarity 98.1° Matches 203; Conservative

Seguence

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PT New inducible expression systems - comprising multi-chimeric transactivator, induces transcription from promoter in the absence of first ligand and presence of second ligand moder in the absence of first ligand and presence of second ligand by the Example 1; Fig 4; 72pp; English.

Example 1; Fig 4; 72pp; English.

Inias is a fusion protein comprising, from N-terminus to C-terminus, the E-coli tetR polypeptide, the transcription activational domain of HSV VP16 and the ligand-binding domain of an oestrogen receptor from pHE14 (Kumar et al. 1986). DNA encoding it can be used as part of an inducible expression system which induces transcription from the promoter in the absence of the first ligand and presence of the compression system requires to promoter in the absence of the inducible expression in cells of polypeptides such as cytotoxic products or therapeutic products. The activation of the inducible expression system requires 1 independent signals, which reduces the incidence of undesired transcriptional activation.
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                                                                                                                                                                                61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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                                            1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIENL
MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML
                                                                                                                                           DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL
                                                                                                                                                                                                                                                                                   121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multi-chimeric transactivator tTAER sequence.
inducible expression system; modulation; cytotoxin; therapeutic;
tTAER; multi-chimeric; transactivator; tetR; Vp16;
ligand-binding domain.
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Pred. No. 5.6e-112;
2; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                           181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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W47583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen ST, Friedmann T, Yee JK; WPI; 98-145597/13.
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98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-1996; US-693940.
(CITY ) CITY OF HOPE.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herpes simplex virus. WO9805754-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-1998.
29-JUL-1997; U13221.
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W47583
AC W47583
AC W47583
AC W47583
AU 11-JUL
DT 21-JUL
OS BESCHALCI
OS WPD 12-FEB
PR 07-FEB
PR 07
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claim 4: Columns 77-80; 63pp; English.

The present sequence is encoded by wild type Inl0-derived tet repressor. It is used in the course of the invention. The specification describes a method for regulating expression of a Tet (tetracycline) operator-linked gene in a cell of a subject. The method comprises introducing into the cell a nucleic acid encoding a fusion protein which inhibits transcription in eukaryotic cells, the fusion protein comprising a polypeptide which hinked to a Tet operator sequence, operatively linked to heterologous second polypeptide which inhibits transcription in eukaryotic cells and modulating the concentration of a tetracycline (analogue) in the subject. The method is used for the regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression system, using tetracycline (analogues). The system enables a gene coupled to the system to be induced in the presence of Tet and then stopped when Tet is removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKOYETLENOLAFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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                                                                                                                                                                                                                                                                                                                                      04-DEC-1998 (first entry)
Protein encoded by wild type Tn10-derived tet repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                          Tet repressor; tetracycline; regulation; expression;
Tet operator-linked gene; tet operator.
181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                       181 GAEPAFLFGLELIICGLEKQLKCESGS 207
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                                                                                                                                                                                                                                                              W71326 standard; Protein; 207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
USS814618-A.
29-SEP-1998.
07-JUN-1995; US-485978.
07-JUN-1995; US-685978.
14-JUN-1993; US-076327.
14-JUN-1994; US-260452.
01-JUL-1994; US-270637.
15-JUL-1994; US-270637.
15-JUL-1994; US-270637.
15-JUL-1994; US-270637.
15-JUL-1994; US-270637.
16-JUL-1994; US-270637.
16-JUL-1994; US-270637.
16-JUL-1994; US-270637.
16-JUL-1994; US-270637.
16-JUL-1994; US-270637.
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RESULT R48630 us-08-486-814-19.rag

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1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
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tTA: tTAS; transactivator; tetracycline-controllable transactivator; conditional inactivation; homologous recombination; gene expression; terasgene regulation; gene therapy; tetracycline-resistance; tetR; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYMHVKNKRALLDALAIEML 60
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                                                                                                                                                                                                                                                                                                                                       Tetracycline repressor-mediated regulation system - useful for controlling gene expression in transgenic animals Disclosure; page 41-42; 76pp. English.

The inventors claim a construct which comprises an animal promoter element having a tetracycline repressor (tetR) operator. The promoter alement may be the PEPCK promoter which is tissue specific shortly prior to birth. The tetR sequence in the construct is 3' to a TATA-box sequence and is inserted into the Nhel site of the PEPCK promoter element. The entire sequence of the tetR sequence 207 AA;
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A DNA fragment of pMSVP16 coding for the C-terminal 97 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1053; DB 1; Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                   Sequence of the tetracycline repressor tetR.
Tetracycline repressor; TetR; Tnl0; transposon 10.
Escherichia coli.
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2; Mismatches
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WPI; 95-036472/05.
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standard; Protein; 207 AA.
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Best Local Similarity 97.6%;
Matches 202; Conservative ;
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                                           (first entry)
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14-JUN-1993; US-076327.
(BADI ) BASF AG.
                                                                                                                                                                            03-MAK-1953.
26-AUG-1993; U08230.
26-AUG-1992; US-935763.
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                                                19-AUG-1994
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Polynucleotide encoding trans.activator fusion protein contg. tet
repressor - used to control expression of gene regulated by minimal
repression is regulated by tetracycline
expression is regulated by tetracycline
bisclosure; Fig 5A-B; 37pp; English.

A fusion protein (R85324) composed of the Escherichia coli In10
tet repressor (tetR) and a 127-amino acid C-terminal portion of the
renscription activating domain of herpes simplex virus virion
protein [6 (vP16)] is the product of novel tetracycline-controlled
transactivator tTA (106868). The transactivator is used to regulate
expression of a heterologous gene operably linked to a minimal promoter
derived iron human cytomegalovirus promoter IE (see 106869-70) and at
least 1 tet operator (tetC) sequence. On/off regulation of expression
of the heterologous protein by host eukaryotic cells is provided by
varying the medium tetracycline conc. Transgenic animals producing
squence 297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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acids of VP16 of HSV was blunted and inserted in pUHD14-1. The resulting plasmid, pUHD151-1, encoded a tetR-VP16 fusion protein, or tetracycline-controllable transactivator (smaller version, tTAS), whose sequence is given in Q76265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transactivator; LTAs; tet repressor; tetR; virion protein 16; VP16; gene expression; tetracycline-responsive promoter;
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                                                                                                                                                                                                                           Length 297;
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Pred. No. 6.7e-112;
2; Mismatches 3;
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Chimeric Herpes simplex virus.
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Best Local Similarity 97.6%;
Matches 202; Conservative
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14-JUN-1993; 076726.
14-JUN-1993; US-076726.
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95-392612/50.
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Matches 202; Conserv
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- 1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
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Search completed: June 9, 1999, 12:59:17 Job time: 9196 sec

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 9, 1999, 12:59:50 ; Search time 19.42 Seconds (without alignments) 399.294 Million cell updates/sec

US-08-486-814-19 1080 1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207 Title: Perfect score: Sequence:

BLOSUM62

Scoring table:

116738 seqs, 37460341 residues Searched:

PIR_58:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

escription	repressor tetR - E	atory protei	atory	cycline resi	etracyclir	atory	protein	repressor	tet repressor - Es	al	S.	cal	tran	probable transcrip	transcription regu	transcription regu	rot	hypothetical prote	on reg	prot	-	glucuronide repres	transcription regu	regu	hypothetical prote		kinesin heavy chai	hypothetical prote	regulatory protein	transcription regu	nuclear migration	transcription regu	iron-dependent rep	in -	~	pha chai	hetical pr	script	conserved hypothet
	RPECTN	807359	S30287	A26948	RPECYS	JQ1478	S38655	RPECR1	I77569	H70740	A40046	A69900	S42419	S42417	C70487	H70042	B70827	E70861	B70391	875298	D64855	D64918	C70035	F70946	S29308	S58095	A41919	C70649	S10899	E69779	S57976	S39744	E69280	C65165	S17885	A35715	H70001	S19095	A64695
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hypothetical prote	probable transcrip	hypothetical prote	hypothetical prote	transcription regu	hypothetical prote
\$12393	E70873	820608	F64100	F69985	238906
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188	187	1391	187	194	190
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	A; Gen C; Sup	ne: to perfar	etR mily:	tetra	acyc]	ine	repr	ess	ssor		
	C; Key F; 25-	/word: -46/Re	s: ant egion:	ibio hel	tic 1 ix-tu	esis urn-h	tanc	. # S	Keywords: antibiotic resistance; DNA binding; transcription 25-46/Region: helix-turn-helix #status predicted	ıon regulation	
	Oue Bes Mat	Query Ma Best Loc Matches	t) is	mila	rity nser	ch 1 Similarity 97.6% 202; Conservative	. 5.8;	2, 5	Score 1053; DB 1; Length Pred. No. 2.2e-91; 2; Mismatches 3; Indels	th 207; els 0; Gaps 0;	
	Qy	1		KSKV 	INSA INSA	CELLN	EVG]	EEGI 	MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 	RALLDALAIEML 60 RALLDALAIEML 60	
	QY	61		HECP - - HECP	LKGE: : - LEGE:	SWODE SWODE	LRNF - - - -	XAKS 	DRHITHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 	QYETLENQLAFL 120 	
	QY	121		SLEN - - SLEN	ALYA 	LSAVG SAVG	HETI ETI	5 - 5	CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 	LLRQAIELFDHQ 180 LRQAIELFDHQ 180	
	Qy	181	GAEPAFLFGLELIICGLEKQLKCESGS	FLFG FLFG	LELI	ICGLE ICGLE	KOL!	KCES HCES KCES	ESGS 207 ESGS 207		
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Willtenate names: tetracycline repressor
C;Species: Salmonella ordonez
C;Species: Salmonella ordonez
C;Accession: S30287
R:Allard, J.D.; Gibson, M.L.; VV, L.H.; Nguyen, T.T.; Bertrand, K.P.
M.I. Gen. Genet. 237, 301-305, 1993
A:Title: Nncleotide sequence of class D tetracycline resistance genes from Salmonella or A;Accession: S30287
S:Clecule type: DNA
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A: Cross-references: EMBL:x65876; NID:g49073; PID:g49075
C: Genetics:
A: Gene: tetR
A: Gene: plasmid
C: Superfamily: tetracycline repressor
C: Keywords: antibiotic resistance; DNA binding; transcription regulation
F: 25-46/Region: helix-turn-helix #status predicted
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                                         A;Molecule type: DNA
A;Residues: 1-218 <UNG>
A;Cross-references: EMBL:X01083; NID:943053; PID:943054
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63.7%; Pred. No. 4.4e-55;
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C.Keywords: antibiotic resistance; DNA binding; tra
F;25-46/Region: helix-turn-helix #status predicted
A; Reference number: S07359; MUID:85037938
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181 DGEQAFLHGLESLIRGFEVQL 201
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                           A; Accession:
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tetracycline resistance protein - Haemophilus parainfluenzae
C;Species: Haemophilus parainfluenzae
C;Species: Haemophilus parainfluenzae
C;Accession: A26948 #sequence_revision 19-Nov-1988 #text_change 12-Jun-1998
R;Heuer, C.; Hickman, R.K.; Curiale, M.S.; Hillen, W.; Levy, S.B.
J. Bacteriol. 169, 990-994, 1987
A;Title: Constitutive expression of tetracycline resistance mediated by a Tn10-like A;Reference number: A26948; MUID:87137315
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C:Species: Escherichia coli

C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 12-Jun-1998

C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 12-Jun-1998

C:Brow, M.A.D.; Pesin, R.; Sutcliffe, J.G

Mol. Biol. Evol. 2, 1-12, 1985

Mol. Biol. Evol. 2, 1-12, 1985
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C.Superfamily: tetracycline repressor
C.Superfamily: tetracycline restance; DNA binding; transcription regulation
E:24-46/Domain: DNA binding #status predicted <DBN>
F:25-46/Region: helix-turn-helix #status predicted
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Query Match

47.4%; Score 512; DB 1; Length 219;
Best Local Similarity 51.7%; Pred. No. 8.9e-41;
Matches 105; Conservative 33; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.3%; Score 597; DB 2; Length 120
92.0%; Pred. No. 4.9e-49;
""" "" "" Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: M15539; NID: 9148988; PID: 9148989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: tetracycline repressor F; 25-46/Region: helix-turn-helix #status predicted
181 GAEPAFLFGLELIICGLEKQL 201
                                                                                  181 DGEQAFLHGLESLIRGFEVQL 201
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A;Cross-references: EMBL:X75761; NID:g415984; PID:g415985
C;Superfamily: tetracycline repressor
F;25-46/Region: helix-turn-helix #status predicted
A; Reference number: S38655
                                                                           A; Residues: 1-216 <TRU>
                 A; Accession: S38655
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                     Query Match
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A:Reference number: JQ1475; MUID:92192465
A:Accession: JQ1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. Cross-references: EMBL:X61367; NID:948194; PID:948198
A. Note: the authors translated the codon GAG for residue 19 as Asp and CAG for residue 8 R. Altschmided, L.; Baumeister, R.; Pfleiderer, K.; Hillen, W.
EMBO J. 7, 4011-4017, 1988
A.Title: A threonine to alanine exchange at position 40 of tet repressor alters the recc A. A. Reference number: S02667; MUID:89091153
A. Accession: S02668
A. Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                          N;Alternate names: tetracycline resistance repressor
C;Species: Escherichia coli
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 12-Jun-1998
C;Accession: JO1478; S02668; S24113
R;Allmeier, H.; Cresnar, B.; Greck, M.; Schmitt, R.
Gene 111, 11-20, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Pseudomonas aeruginosa
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMP--PLLRQAIELFD 178
               61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                              CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERE----TPTTDSMPPLLRQAIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                           regulatory protein tetR - Escherichia coli transposon In1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.8%; Score 505.5; DB 2; 51.5%; Pred. No. 3.5e-40;
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A;Residues: 1-100 <ALT>
C;Genetics:
A;Gene: tetR
C;Superfamily: tetracycline repressor
F;25-46/Region: helix-turn-helix #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Mismatches
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                                                                                                                                                                           177 FDHQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                   179 HQGAEPAFLFGLELIICGLEKQ 200
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Best Local Similarity
Matches 104; Conserv
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tet repressor protein (Tn 1721) - Escherichia coli plasmid RP1
C;Species: Escherichia coli
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 12-Jun-1998
C;Accession: A03574
R;Waters, S.H.; Rogowsky, P.; Grinsted, J.; Altenbuchner, J.; Schmitt, R.
Nucleic Acids Res. 11, 6089-6105, 1983
A;Titler The tetracycline resistance determinants of RP1 and Tn1721: nucleotide seque
A;Reference number: A93486; MUID:83299270
                                                        5;
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                                                                                                                                                                                                                                                                             61 AENHTHSVPRADDDWRSFLIGNARSFRQALLAYRDGARIHAGTRPGAPQMETADAQLRFL 120
                                                                                                                                                                                                                                                                                                                                   121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMP--PLLRQAIELFD 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: tetracycline repressor
C;Keywords: antibiotic resistance; DNA binding; transcription regulation
F;25-46/Region: helix-turn-helix #status predicted
                                                                                                                                          1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.9%; Score 495.5; DB 1; Length 216; 50.5%; Pred. No. 3.1e-39; Live 36; Mismatches 61; Indels 3
  Length 216;
     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-216 <MAT>
A;Cross-references: GB:X00006; NID:942508; PID:942509
                         .5e-40;
        DB
46.8%; Score 505.5;
51.5%; Pred. No. 3.5e
tive 35; Mismatches
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                            Best Local Similarity 51.5%
Matches 104; Conservative
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Matches 102;
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PESULY 9	Db 76 VFATPYIEAGDWRETLRNHARSMRKTFADNPVLCDLILIRAALSPKTARLGA 128
11/209 11/209 12/20prissor - Escherichia coli 7.Sperios: Ferbarichia coli	QY 106 TERQYETLENQLAFLCQQGFSLENALYALSAVGHFTLGCYLEDQE 150
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 12-Jun-1998 C;Accession: 177569	Db 128QEMERAIANLVTAGLSLEDAFDIYSAVSVHVRGSVVLDRLSRKSQSAGSGPSAIE 182
R;Tovar, K.; Ernst, A.; Hillen, W. Mol. Gen. Genet. 215, 76-80, 1988 A;Title: Identification and nucleotide sequence of the class E tet regulatory elements a A;Reference number: 157766; MUID:89201249	OY 151 HQVAKEERETPTIDSMPPLLRQAIELFDHQCAEPAFLFGLELII 194
Fracessium: 1/7009 ** Fracessium: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA	RESULT 11
A;Residues: 1-211 <res> A;Cross-references: EMBL:X14035; NID:g43055; PID:g43056 C;Superfamily: tetracycline repressor</res>	TetR repressor homolog actII-1 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 12-Jun-1998
cus predicted	
Query Marcn Query Marcn Best Local Similarity 50.2%; Pred. No. 4.6e-39; Matches 101; Conservative 29; Mismatches 68; Indels 3; Gaps 1;	A;Title: The act cluster contains regulatory and antibiotic export genes, direct targ A;Reference number: A40046; MUID:91347376 A;Accession: A40046
QY 1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60	A; Molecule type: UNA A; Residues: 1-259 <fer> A; Cross-references: GB:M64683; NID:9153143; PID:9455360 C; Genetics:</fer>
QY 61 DRHHTHFCPLKGESWODFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120 :	A;Start codon: GTG F;52-73/Region: helix-turn-helix #status predicted
QY 121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180 	Query Match 13.7%; Score 147.5; DB 2; Length 259; Best Local Similarity 26.0%; Pred. No. 1.3e-06; Matches 57; Conservative 35; Mismatches 90; Indels 37; Gaps 8;
	QY 4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAI 57 : ::: : : ::: : : : : : Db 31 LTQDRIVVTALGILDAEGLDALSMRRLAQELKTGHASLYAHVGNRDELLDLVFDIVLTEV 90
SULT 10	QY 58 EMLDRHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPT-EKQYETLENQ 116 :
hypothetical protein Rv1353c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998	QY 117 LAFLCQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERET 160 :
GOI	QY 161 PTTDSMPPLLRQAIELFDHQGAEPAFLFGLELIICGL 197
Taylor, N. Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987	RESULT 12 A69900
A;Accession: H70740 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA	hypothetical protein yobs - Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1998
A; Residues: 1.261 <col/> A; Cross-references: GB:275555; GB:AL123456; NID:g3261608; PID:e250355; PID:g1419056 A; Experimental source: strain H37Rv C; Genetics: A; Gene: Rv1353c	C; Accession: A69900 R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Arinich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
ore 168.5; DB 2; Length 261; ed. No. 1.5e-08;	A.Authors: Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Gh Wood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Laube A; Authors: Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Med
MACCIES 01; CONSEIVALIVE 32; MISMACCIES /8; INDELS 55; GAPS 6; QY 4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRH 63 :: :: : :	, K.; Oglwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Por Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schl A; Authors: Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Ser amakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vanden ; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasa, K.; Yata, K.; Yoshida, K.; Yoshikaw
Qy 64 HTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRP 105	A; Authors: Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili

156 DLDKETAVIF 165

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probable transcription repressor mtrR - Neisseria gonorrhoeae (strain CH95)
C; Species: Neisseria gonorrhoeae
A; Variety: strain CH95
C; Date: (O'May-1998 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
C; Date: (O'May-1998 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
C; Accession: 842417, 840251
Mol. Microbiol. 11, 769-775, 1994
A; Title: Regulation of the permeability of the gonococcal cell envelope by the mtr sy A; Reference number: 842417
A; Reference number: 842417
A; Retence number: 942417
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Cross-references: EMBL: 225796; NID: 9438190; PID: 9438191
A; Experimental source: CH95
C; Genetics:
A; Gene mtrR
C; Superfamily: probable transcription regulation
C; Keywords: DNA binding; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUD:98196666 A;Accession: C70487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-192 <AQF>
A;Residues: 1-192 <AQF>
A;Crossreferences: GB:AEO00776; NID:q2984355; PID:g2984362; GB:AEO00657
A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription regulator TetR/AcrR family - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998
C;Accession: C70487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 EH--TEQNA--AVIAIA------RKHQAIWREKIT------AVLTEAVENQDLAD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 CIAQDAADAEGGSWTVF-RHTLLHFFERLQSNDIYYKFH--------NILFLKC 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 ----HFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFLC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 KEHLMLAALETFYRKGIARTSLNEIAQAAGVTRGALYWHFKNKEDLFDALFQRICDDIEN 71
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9.6%; Score 103.5; DB 2; Length 192;
Best Local Similarity 22.7%; Pred. No. 0.012;
Matches 45; Conservative 35; Mismatches 67; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.8%; Score 105.5; DB 2; Length 210;
Best Local Similarity 26.8%; Pred. No. 0.0086;
Matches 51; Conservative 23; Mismatches 73; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 HQGAEPAFLF 188
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C;Species: Neisseria gonorrhoeae
A;Variety: strain FA19
C;Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
C;Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
C;Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 18-Sep-1998
C;Accession: 542419
A;Title: Regulation of the permeability of the gonococcal cell envelope by the mtr syste
A;Accession: 542419
                                                                                                      A;Molecule type: DNA
A;Residues: 1-191 <KUN>
A;Cross-references: GB:299114; GB:AL009126; NID:92634230; PID:e1185379; PID:92634300
A;Experimental source: strain 168
C;Genetics:
A;Gene: yobS
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ω
A;Reference number: A69580; MUID:98044033
A;Accession: A69900
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 LDRHHTHFCPLKGES------WQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYE 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 IVSDQIVCLVTK-LLIENGYASEKTAIHATRGLRSLLHGFTVLIAKEAFEREEDILESLS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 TLENQLAFICQQGFSLENALYALSAVGHFTLG--CVLEDQEHQVAKE--ERETPTTDSMP 167
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9.9%; Score 106.5; DB 2; Length 210;
Best Local Similarity 26.8%; Pred. No. 0.0069;
Eatches 51; Conservative 23; Mismatches 73; Indels 43
                                                                                                                                                                                                                                                                                                                                                             ch 11.4%; Score 123; DB 2; Length 191; I Similarity 24.1%; Pred. No. 0.00018; 49; Conservative 38; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-210 <PAN>
A:Cross-references: EMBL:Z25797; NID:g452332; PID:g438189
A:Experimental source: strain FA19
C:Genetics:
A:Gene mirR
C:Superfamily: probable transcription repressor mtrr
C:Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 PLLRQAIELFDHQGAEPAFLFGL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 FSIR-----TFLSGL 183
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Best Local Similarity
Matches 49; Conserva
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Gaps

43;

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Search completed: June 9, 1999, 12:59:50 Job time: 9169 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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- protein search, using sw model OM protein 9, 1999, 13:01:02; Search time 16.52 Seconds (without alignments) 336.316 Million cell updates/sec June Run on:

Perfect score: Title:

US-08-486-814-19 1080 1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207 Sequence:

BLOSUM62 Scoring table: 74019 seqs, 26840295 residues Searched:

SwissProt_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	483 escheri	pa	pasteur			escher	escheri		=	P39897 neisseria g	w	Q59431 escherichia							Q13813 homo sapien																	esch	sns	_	_	ž.	P34402 caenorhabdi	25 gallus gal)1 ga
SUMMAKIES	QI	TER2_	TER8_	TER8_	TER4_	TER3_	TERI	TER	-	X071	MTRR			PHSL		KINH	BETI		TIK				N15			-	•	_	•					_	FA8_	_	ATKA	•		_				HS9A
	Query Match Length DB	207		207	217	219	216	211	210	261	210	236	196	955	577	963	195	299	212	2472	549	188		187	770	218	215	519	212	192	2748	673	838	1324	2319	1509	557	2133	474	2116	892	1207	323	728
æ	Query Match	97.	ø	61	61	47	46	45	43	15	σ	œ	80	80	7	7	7	7	7	7	_	_	7	_	~	_	_	7	_	_	7	-	-	w	u	•	•	_	_	w	•	v	•	
	Score	1053	665	663	099	512	505.5	o	473	w	106.5	92.5	91.5	86	84.5	83.5	83	82.5	82	81.5	80.5	80	79.5	79	78.5	78.5	78	78	77.5	77	77	77	76.5	75	75	75	74.5	74	74	74	74	74	73.5	73.5
,	Result No.	1	7	m	4	S	Q	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	36	40	4.1	42	4.3

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PO8238 homo sapien
P75342 mycoplasma
 HS9B_HUMAN
 - -
 723
1244
 8.8
9.8
 73.5
  44
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ALIGNMENTS

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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                    SMITH L.D., BERTRAND K.P.;
J. MOL. BIOL. 203:949-959(1988).

J. MOL. BIOL. 203:949-959(1988).

I. MOL. BIOL. 203:948-959(1988).

ELEMENT, ITS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE ELEMENT, ITS AMINO-TERMINAL REGION FORMS A HELLX-TURN-HELLX STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES (TETA) PROMOTER OPERATOR SITES.

-1- SIMILARITY: BELONGS TO THE TETRACKEN FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H->Y: REDUCES AFFINITY FOR TETRACYCLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N->H: REDUCES AFFINITY FOR TETRACYCLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T->1: REDUCES AFFINITY FOR TETRACYCLINE LESS THAN 10 FOLD.
4AB4DD5A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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INVOLVED IN BINDING TO [MG-TC]+ (BY
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Pred. No. 3.4e-92;
2; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS B (TRANSPOSON IN10).
                                                                                                                                                                                                                    MEDLINE; 84005886.
BERTRAND K.P., POSTLE K., WRAY L.V. JR., REZNIKOFF W.S.;
GENE 23:149-156(1983).
                      207 AA
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                                                                                                                                                                      POSTLE K., NGUYEN T.T., BERTRAND K.P.;
NUCLEIC ACIDS RES. 12:4849-4863(1984).
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97.6%;
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                        STANDARD;
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                                                                                                                             ENTEROBACTERIACEAE
                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 84247342.
                                                                                                                                                                                                                                                                   MUTAGENESIS.
MEDLINE; 89094871.
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                      TER2_ECOLI
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RESULT 1
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UNGER B., KLOCK G., HILLEN W.;
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                                                                                                                                                                                                 PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
           MICROBIOL. IMMUNOL. 38:31-38(1994).

-!-FUNCTION: TETR TEPRESSOR OF THE TETRACYCLINE RESISTANCE ELEMENT; ITS AMINO-TERINESSOR FORMS A HELIX-TURN-HELIX STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE (TETA) PROMOTER OPERATOR SITES.
-!-INDUCTION: BY THE [MG-TETRACYCLINE] + COMPLEX.
-!-INDUCTION: BY THE [MG-TETRACYCLINE] + COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                          H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                                                                                                                                        MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY SIMILARITY).
3C57D4AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.6%; Score 665; DB 1; Length 218; 63.7%; Pred. No. 1.2e-55; Live 27; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                 EMBL, D16172; G575938; -. PROSITE; PS01081; HTH_TETR_FAMILY; 1. TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
                                                                                                                              01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS H.
                                                                                                              218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                      181 GAEPAFLFGLELIICGLEKQLKCESGS 207
                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                ANTIBIOTIC RESISTANCE; PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
TER8_PASMU STANDARD; F
AC P51561;
DT 01-OCT-1996 (REL. 34, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                         218 AA; 24419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GAEPAFLFGLELIICGLEKQL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 DGEQAFLHGLESLIRGFEVQL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 128; Conservative
                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                             45
64
                                                                                                                                                                               PASTEURELLA PISCICIDA.
                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 94328963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                            PASTEURELLACEAE
                                                                                                                                                                                        PLASMID PSP935
                                                                                                                                                                                                                                                                                                                                        REGULATORS
                                                                                                            ER8_PASPI
                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                        RESULT 2
TER8_PASPI
                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
                                                           181
                  g
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; PASTEURELLACEAE.
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HANSEN L.M., MCMURRY L.M., LEVY S.B., HIRSH D.C.;
ANTIMICROB. AGENTS CHEMOTHER. 37:2699-2705(1993).

-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT; ITS AMINO-TERMINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
(TETA) PROMOTER OPERATOR SITES.
-!- INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
-!- SIMILARITY: BELONGS TO THE TETRACYCLINE] OF TRANSCRIPTIONAL
REGILATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSM--PPLLRQAIELFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGNESIUM (OF [MG-TC]+ COMPLEX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.4%; Score 663; DB 1; Length 207; 63.2%; Pred. No. 1.7e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U00792; G392872; -
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
ANTHEIOTIC RESISTANCE; PLASMID BNA_BIND 26 H-T-H MOTTF / POTERWIT
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A51DA28B CRC32;
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01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES-E.COLI; STRAIN=J53-1; PLASMID=RA1;
MEDLINE; 85037938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESCHERICHIA COLI, AND SALMONELLA ORDONEZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TETRACYCLINE REPRESSOR PROTEIN CLASS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 HQGAEPAFLFGLELIICGLEKQLK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |||| |:::| ||| || 1| 1| 1| 1| 1| SDNGDAAFLEVLDVMISGLETVLK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 AA; 23156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                     PASTEURELLA MULTOCIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  MEDLINE; 94153051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100
                                                                                                                                  PLASMID PVM111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TER4_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TER4_ECOLI
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SEQUENCE FROM N.A.
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P03038;
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        MEDLINE;
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PLASMID PSC101.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                         122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQG 181
                                                                                                                                                                                                                                                                                                                                                                                                                               62 RHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFLC 121
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLD 61
                                                                                                                                                                           -:- INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
-:- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                           HINRICHS W., KISKER C., DUEVEL C., MUELLER A., TOVAR K., HILLEN
                                                                                                                                                                                                                                                                                                                                                                          ..
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                                             ALLARD J.D., GIBSON M.L., VU L.H., NGUYEN T.T., BERTRAND K.P.;
MOL. GEN. GENET. 237:301-305(1993).
                                                                                                                                                                                                                                                                                               H-T-H MOTIE (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+.
MAGNESIUM (OF [MG-TC]+ COMPLEX).
830EPSEE CRG32;
                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS), AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      61.1%; Score 660; DB 1; Length 217; 63.5%; Pred. No. 3.5e-55;
                                                                                                                                                                                                                                                   PDB: 2TRT; 20-JUN-96.
PROSITE: PSO1081: HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGILATION; REPRESSOR; DNA-BINDING; PLASMID;
ANTIBIOTIC RESISTANCE; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                          46; Indels
                  SEQUENCE FROM N.A.
SPECIES-S.ORDONEZ; STRAIN-BM2000; PLASMID-PIP173;
MEDLINE; 93204906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 AA
                                                                                                                                                                                                                                                                                                                                                                          27; Mismatches
NUCLEIC ACIDS RES. 12:7693-7703(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (REL. 01, CREATED)
                                                                                                                                                                                                                                                                                                                             217 AA; 24287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GEOAFLHGLESLIRGFEVOL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 AEPAFLFGLELIICGLEKQL 201
                                                                                                                                                                                                                                                                                                                                                                           Matches 127; Conservative
                                                                                                                                                                                                      EMBL; X01083; G43054; -. EMBL; X65876; G49075; -. PIR; S07359; S07359. PIR; S30287; S30287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                           PDB; 2TCT; 03-APR-96.
PDB; 2TRT; 20-JUN-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                   MEDLINE; 94204640
                                                                                                                                                                                               REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TER3_ECOLI
P03039;
                                                                                                                                                                                                                                                                                         INIT_MET
DNA_BIND
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         Query Match
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PLASMID RP1, AND PLASMID RP4.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERE----TPTTDSMPPLLRQAIEL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BROW M.A.D., PESIN R., SUTCLIFFE J.G.;
MOL. BIOL. EVOL. 2:1-12(1985).
-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT; ITS ANINO-TEMBINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                       (TETA) PROMOTER OPERATOR SITES.
SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML
                                                                                                                                                                                                                                                                                                                                                                                        H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
SIMILARITY).
MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 219;
                                                                                                                                                                                                                                  EMBL; M36272; G150946; -.
PIR; A03575; REPECYS.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING; PLASMID;
ANTIBIOTIC RESISTANCE.
DNA_BIND 26 45 H-T-H MOTIF (POTENTIAL).
SITE 64 1 INVOLVED IN RINDING TO MA-FTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (REL. 01, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS A (TRANSPOSON 1721).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
6C9E1828 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.4%; Score 512; DB 1;
51.7%; Pred. No. 3e-41;
tive 33; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLMEIER H., CRESNAR B., GRECK M., SCHMITT GENE 111:11-20(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
PLASMID=PLASMID RP4;
TRUEMAN P., SHARPE G.S., BARTH P.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 FDHQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VYEGGPDAAFERGLALIIGGLEK 203
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TRANSPOSON-TN1721; PLASMID-RP1;
MEDLINE; 83299270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 AA; 24174 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100
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MEDLINE; 92192465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
88216101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESCHERICHIA COLI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMP--PLLRQAIELFD 178
WATERS S.H., ROGOWSKY P., GRINSTED J., ALTENBUCHNER J., SCHMITT R.;
NUCLEIC ACIDS RES. 11:6089-6105(1983).
-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT; ITS AMINO-TERNINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CEAGFSAGDAVNALMIISYFTVGAVLEEQAGDSDAGER-GGTVEQAPLSPLLRAAIDAFD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOVAR K., ERNST A., HILLEN W.;
MOL. GENET. 215.76-80(1988)
-!- FUNCTION: TETR REPRESSOR OF THE TETRACYCLINE RESISTANCE
ELEMENT, ITS AMINO-TERRINAL REGION FORMS A HELIX-TURN-HELIX
STRUCTURE AND BINDS DNA. BINDING OF TETRACYCLINE TO TETR REDUCES
THE REPRESSOR AFFINITY FOR THE TETRACYCLINE RESISTANCE GENE
                                                                                          (TETA) PROMOTER OPERATOR SITES.
-!- INDUCTION: BY THE [MG-TETRACYCLINE]+ COMPLEX.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TETA) PROMOTER OPERATOR SITES.
SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                      INVOLVED IN BINDING TO [MG-TC]+ (BY
                                                                                                                                                                                                                                                                                                     SIMILARITY),
MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                            46.8%; Score 505.5; DB 1; Length 216; 51.5%; Pred. No. 1.2e-40;
                                                                                                                                                                                                  PIR; A03574; RPECRI.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; TRANSPOSABLE ELEMENT;
DNA-BINDING; ANTIBIOTIC RESISTANCE; PLAMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60; Indels
                                                                                                                                                                                                                                                                                                                                 SIMILARITY).

TH -> ST (IN REF. 3).

I -> T (IN REF. 3).

DA -> ES (IN REF. 3).

#; F72BDFB1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Mismatches
                                                                                                                                                                                                                                                                       H-T-H MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 HQGAEPAFLFGLELIICGLEKQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : || || : || |: || || 180 EAGPDAAFEQGLAVIVDGLAKR 201
                                                                                                                                                                                                                                                                                                                                                              80
155
23320 MW;
                                                                                                                                                         EMBL; X61367; G48198; -.
EMBL; X75761; G415985; -.
EMBL; X00006; G42509; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                              65
80
154
216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 89201249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                             REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLASMID PSL1503
                                                                                                                                                                                                                                                   DNA-BINDING;
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TERS_ECOLI P21337;
                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                METAL
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PLASMID PJA8122.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                  61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
                                                                                                                                                                                                                                                                                                                                                                      121 CQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIELFDHQ 180
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                            1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MICROBIOL. IMMUNOL. 36:1051-1060(1992).

-!- FUNCTION: TETR IS THE REPRESSOR OF THE TETRACYCLINE RESISTANCE ELEMENT; ITS AMINO-TERMINAL REGION FORMS A HELLY-TURN-HELLY STRUCTURE AND BIRDS DAY. BINDING OF TETRACYCLINE TO TETR REDUCES (TETA) PROMOTER OPERATOR SITES.

-!- INDUCTION: BY THE [MG-TETRACYCLINE] + COMPLEX.

-!- SIMILARITY: BELONGS TO THE TETRACYCLINE OF TRANSCRIPTIONAL
                                                                               H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY SIMILARITY).
                                                                                                                       MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H-T-H MOTIF (POTENTIAL).
INVOLVED IN BINDING TO [MG-TC]+ (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAGNESIUM (OF [MG-TC]+ COMPLEX) (BY SIMILARITY).
                                                                                                                                                                                                                                      .,
ښ
                                                                                                                                                                                                     45.7%; Score 493.5; DB 1; Length 211; 50.2%; Pred. No. 1.6e-39; tive 29; Mismatches 68; Indels 3;
        EMBL; M34933; G155020; ALT_SEQ.
EMBL; X14035; G43056; -.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S52438; G262929; -.
PROSITE: PS01081; HTH_TETR_FAMILY; 1.
TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING;
ANTIBIOTIC RESISTANCE; PLASMID.
DNA_BIND 26 45
                                                                                                                                                    V -> L (IN G43056).
F538C813 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TETRACYCLINE REPRESSOR PROTEIN CLASS G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              811CB332 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                ANTIBIOTIC RESISTANCE; PLASMID.

DNA_BIND 26 45 H-
                                                                                                                                                                                                                                                                                                                                                                                                                                             178 SAEMAFHFGLKSLIFGFSAQL 198
                                                                                                                                                                                                                                                                                                                                                                                                                          181 GAEPAFLFGLELIICGLEKQL 201
                                                                                                                                                                211 AA; 23585 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 AA; 23595 MW;
                                                                                                                                                                                                                               Matches 101; Conservative
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                                                                                                                       100
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MEDLINE; 93125225.
ZHAO J., AOKI T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                       100
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REGULATORS.
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P51560;
                                                                                                                                                 CONFLICT
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                     Best Local
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                                                                                                                         METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 HTHFCPLKGESWQDFLRNKAKSFR------CALL-----SHRNGAKVHSDTRP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 VFATPYIEAGDWRETLRNHARSMRKTFADNPVLCDLILIRAALSPKTARLGA----- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 TEKQYETLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQ-------E 150
                                                                                                                            121 COOGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPP--LLRQAIELFD 178
                                                                                                                                                                                 121 CAEGFCPKRAVWALRAVSHYVVGSVLEQQASDADERVPDRPDVSEQAPSSFLHVLFHELE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRH 63
                                            Gaps
                                                                 1 MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                               MURRHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55;
                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 27.0%; Pred. No. 7.8e-09;
Matches 61; Conservative 32; Mismatches 78; Indels 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: Z7555; E250355; -.
PROSITE; PS01081; HTH_TERR_FAMILY; FALSE_NEG.
PROSITE: PS01081; HTH_TERR_FAMILY; FALSE_NEG.

PROSITE: PS01081; HTH_TERR_FAMILY; FALSE_NEG.

BNOTHETICAL PROTEIN; TRANSCRIPTION EGULATION; DNA-BINDING.
BNA_BIND
BNA_BIND
SEQUENCE 261 AA; 28253 MW; BCBECC98 CRC32;
                     Score 473; DB 1; Length 210;
Pred. No. 1.3e-37;
                                                                                                                                                                                                                                                                                                                                                                         MYCOBACTERIUM TUBERCULOSIS.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                            72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 HQVAKEERETPTTDSMPPLLRQAIELFDHQGA--EPAFLFGLELII 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR CY02B10.17C.
            43.8%; Scott
y 47.3%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 AA.
                                                                                                                                                                                                                                                                                        261 AA
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                           179 HQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                                        181 TDGMDAAFNFGLDSLIAGFER 201
                       Query Match
Best Local Similarity 47.38
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-H37RV;
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P39897;
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ID YO7H MYCTU
                                                                                                                                                                                                                                                                                                   011023;
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MTRR_NEIGO
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SEQUENCE FROM N.A.
STRAIN-K12 / MOIGS5;
BLAITHER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H-T-H MOTIF (POTENTIAL).
H -> Y: IN PENICILLIN-RESISTANT ISOLATES.
;, F4CABF98 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 CIAQDAADAEGGSWIVF-RHILLHFFERLQSNDIHYKFH------NILFLKC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIE---LFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 ----HFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFLC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 KEHIMLAALETFYRKGIARTSLNEIAQAAGVTRGALYWHFKNKEDLFDALFORICDDIEN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN NDH-MFD INTERGENIC REGION
                                                                                                                     NEISSERIA GONORRHOEAE.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 26.8%; Pred. No. 0.0041;
Matches 51; Conservative 23; Mismatches 73; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000211; G1787354; -. ECOGENE: EG13435; YCFQ. PROSITE; PS01081; HTH_TETR_FAMILY; FALSE_NEG. HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; REPRESSOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, 225/97; G438189; -.
PIR; S40250; S40250.
PROSITE; PS01081; HHH_TETR_FAMILY: 1.
TRANSCRIPTION REGULATION; DNA-BINDING; REPRESSOR.
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
REGULATORY PROTEIN MTRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 AA; 24192 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATORS.
                                                                                                                                                                NEISSERIACEAE.
                                                                                                                                                                                                                                         STRAIN-FA19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCFQ_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
VARIANT
SEQUENCE
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DNA-BINDING

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66 HFC-PLKGESWQDFL 79
                                               73 RFREPIEGIHFVDYM 87
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THT1_SCHPO
ID THT1_SC
AC 009684,
DT 01-NOV
DT 01-NOV
DT 01-NOV
DE NUCLEAE
                                                                                                  PHSL_IPOBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
RASHIMOTO K., KIM S., KIMORA S., KITAGAWA M., KITAKAWA M., MAKINO K.,
MASUDA S., MIKI T., MAZOBUCHI K., MORIH H., MOTOMURA K., NAKAMURA Y.,
NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMEEI G., SEKI Y.,
TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;
SUBMITTED (DEC-1996) TO EMBL/GENDANK/DDBJ DATA BANKS.
-- FUNCTION: REPRESSOR FOR THE UIDRABC (GUSRABC) OPERON.
                                                                                                                                                                                                                                                                                                                                                                                         ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLATINER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.I., GLASNER F.D., SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                            46 DRDAALDKAMKLFWQHGYEATSLADLVEATGAKAPTLYAEFTNKEGLFRAVLDRYIDRFA 105
                                                                                                                                                      63 --HHTH-FCPLKG--ESWQDFLRNKAKSF------RCALLSHRNGAKVHSDTR 104
                                                                                                                                                                               106 AKHEAOLFCEEKSVESALADYFAAIANCFTSKDTPAGCFMINNCTTLSPDSGDIANTLKS 165
                                                                                                   5 DKSKVINSALELLNEVGIEGLITTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDR-- 63
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                 Query Match
8.6%; Score 92.5; DB 1; Length 236;
Best Local Similarity 25.2%; Pred. No. 0.098;
Matches 35; Conservative 18; Mismatches 63; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 91.5; DB 1; Length 196;
24.0%; Pred. No. 0.097;
Live 24; Mismatches 32; Indels
  H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12;
WILSON K.J., JEFFERSON R.A.;
SUBMITTED (OCT-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-T-H MOTIF (POTENTIAL).
6C1840FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000257; G1787904; -.
EMBL; D90805; G1742672; -.
ECOGENE; EG12667; UIDR.
PROSTE; PSO1081; HTH TETR FAMILY; 1.
TRANSCRIPTION REGULATION; DNA-BINDING; REPRESSOR.
  86 H-T-H MOTIF (PUTE)
26204 MW; ADIF64FC CRC32;
                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                UID OPERON REPRESSOR (GUS OPERON REPRESSOR).
                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (REL. 35, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 52 F
196 AA; 21799 MW;
                                                                                                                                                                                                         105 PTEKQYETLENQLAFLCQQ 123
                                                                                                                                                                                                                                 166 RHAMQERTLQQ---FLCQR 181
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M14641; G868019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
BLATINER F.R., PLUNKE
 67
236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             UIDR OR GUSR
                                                                                                                                                                                                                                                                                                UIDR_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12
DNA_BIND
SEQUENCE
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SEQUENCE
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CARBOHYDRATE METABOLLSM. ENZYMES FROM DIFFERENT SOURCES DIFFER IN THEIR REGULATORY MECHANISMS AND IN THEIR NATURAL SUBSTRATES. HOWEVER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00102; PHOSPHORILASE; 1.
TRANSFERASE; GLYCOSYLITRANSFERASE; CARBOHYDRATE METABOLISM;
ALLOSTERIC ENZYME; PYRIDOXAL PHOSPHATE; TRANSIT PEPTIDE; CHLOROPLAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches 67; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 KNKRALLDALAIEMLDRHHTHFCPLKGESWQDFLRNK-----AKSFRCALLSHRNGAKVH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KNEGTLLDAASIASSIKYHAEFSP--AFSPERFELPKAYFATAQSVRDALIVWWNA---- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 SDTRPTEKQYETLENQLAFLCQ----QGFSLENALYALSAVGHFT-----LGCVLEDQEH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: (1,4-ALPHA-D-GLUCOSXL)(N) + ORTHOPHOSPHATE = (1,4-ALPHA-D-GLUCOSXL)(N-1) + ALPHA-D-GLUCOSE 1-PHOSPHATE.
-! COFACTOR: PYILDOXAL PHOSPHATE.
-!- SUBCELLULAR LOCATION: CHLOROPLAST, AWYLOPLAST.
-!- SIMILARITY: BELONGS TO THE GLYCOGEN PHOSPHORYLASE FAMILY.
EMBL; M64362; G168276; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSRL------DKSKVINSALELLNEVGIEGL--TTRKLAQKLGV-EQPTLYWHV--- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSRLSGITPRARDDRSQFQNPRLEIAVPDRTAGLQRTKRTLLVKCVLDETKQTIQHVVTE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLOROPLAST (POTENTIAL).
ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME.
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
W; 86E3D50F CRC32;
                                                                                                                                                                                                                                                                                                                                 LIN C.T., YEH K.W., LEE P.D., SU J.C., PLANT PHYSIOL. 0:0-0(1992).
                                                                                                                                                               (STARCH PHOSPHORYLASE L).
IPOMOEA BATATAS (SWEET POTATO) (BATATE).
EURARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
                                               01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (EC 2.4.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.0%; Score 86; DB 1; Length 955; 30.1%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THII_SCHPO STANDARD; PRT; 577 AA. 009684; C1-NOY-1995 (REL, 32, CREATED) 01-NOY-1997 (REL, 35, LAST SEQUENCE UPDATE) 01-NOY-1997 (REL, 35, LAST ANNOTATION UPDATE) NUCLEAR FUSION PROTEIN THII.
     955 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            955 AA; 108520 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMYLOPLAST; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                    SOLANALES; CONVOLVULACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 30.19
les 56; Conservative
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43
955
801
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPERTIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 -VASKE 171
PHSL_IPOBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWQD--FLRNKAKSFRCALLSH-RNGAKVHSDTRPTEKQYET----------------113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 SFKDINFRVNQEIMGLVELQNHQQEGMVQQKEILSTIKQLKSEIFDINSFFANFIEESAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 LENQLAFICQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEER----ETPTTDSMPP 168
                                                                                                                                                                                                                                                                                                                                                                     37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    14 LELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHTHFCPLKGE 73
                                                                                                                                                  DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 94242426.
NICLAS J., NAVONE F., HOM-BOOHER N., VALE R.D.;
NEURAN 12:1059-1072(1994).
-i- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAYONE F., NICLAS J., HOM-BOOHER N., SPARKS L., BERNSTEIN H.D., MCCAFEREY G., VALE R.D.;
J. CELL BIOL. 117:1263-1275(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                      Ouery Match
7.8%; Score 84.5; DB 1; Length 577;
Best Local Similarity 24.0%; Pred. No. 1.6;
Matches 49; Conservative 35; Mismatches 83; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KULL F.J., SABLIN E.P., LAU R., FLETTERICK R.J., VALE R.D.;
NATURE 380:550-555(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) KNSI OR KNS.
                                                            SEQUENCE FROM N.A.
IANGE Y., HORIO T., SHIMANUKI M., TANAKA K., NIWA O.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
THT1 OR SPAC13C5.03.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1-349.
MEDLINE; 96195066.
                                                                                                                                                                                                                                                                             POTENTIAL.
697D09FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1993 (REL. 27, CREATED)
01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      963 AA
                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 SVQSNID-FVNSGFQPLYDLTIQL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 LLRQAIELFDHQGAEPAFLFGLEL 192
                                                                                                                                                                                              EMBL; D87337; G1526454; -. EMBL; Z50112; G908892; ALT_INIT.
                                                                                                                                                                                                                                                                                           66972 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                              425
454
                                                                                                                                                                                                                                                                              491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                             471 4
577 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PLACENTA;
MEDLINE; 92299683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              405
                                                                                                                                                                                                                                 TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINH_HUMAN
P33176;
                                                                                                                                        STRAIN=972;
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                  FRANSMEM
                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
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CC --- SUBGRIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT CHAINS CLICOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT CHAINS CLICOMER COMPOSED OF TWO HEAVY CHAINS AND THE PROCESSES IN THE NEURONS:

--- SUBGELLULAR LOCATION: UNIFORMLY DISTRIBUTED BETWEEN THE CELL BODY CC --- DOWAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR N-CC TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF ALPHA-HELICAL COLLED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION; AND A SMALL GLOBULAR C-TERMINALD DOMAIN WHICH AS THE KINESIN LIGHT CHAINS).

CC INTERACTS WITH OTHER PROPERINS (SUCH AS THE KINESIN LIGHT CHAINS).

CC INTERACTS WITH OTHER PROPERINS (SUCH AS THE KINESIN LIGHT CHAINS).

CC INTERACTS WITH OTHER PROPERINS (SUCH AS THE KINESIN LIGHT CHAINS).

CC INTERACTS WITH OTHER PROPERINS (SUCH AS THE KINESIN LIGHT CHAINS).

CC INTERACTS WITH OTHER PROPERINS (SUCH AS THE KINESIN LIGHT CHAINS).

CC INTERACTS WITH MEMBRANOUS ORGANELLES.

CO SUBFAMILY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN AND BOUT BRAILY. KINESIN MICROTUBULES; AND MEMBRANOCHEMICAL (MOTOR) (BY SIMILARITY).

EMBL: X65873; G34083; --

DR PRIS, A41919; MICROTUBULES; APPENDINING; COLLED COIL.

WM ONTOR PROTEIN; MICROTUBULES; APPENDINING; COLLED COIL.

FT DOMAIN 329 914 COLLED COIL.

FT DOMAIN 329 914 COLLED COIL.

FT DOMAIN 915 963 GLOBULAR.

FT DOMAIN 915 963 GLOBULAR.

FT DOMAIN 915 963 MA; 7C040109 CRC32;
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308 NESETKSTLLFGQRAKTIKNTVCVNVELTAEOWKKKYEKEKEKNKILRNTIQWLENELNR 367
                                                                                                                                                                                                                                              93 HRNGAKVHSDTRPTEKQYETLENQL-AFLCQQGFSLEN--ALYALSAVGHFTLGCVLEDQ 149
                                                                                                                          248 LDEAKNINKSLSALGNVISALAEGSTYVPYRDSKMTRILQDSLGGNCRTTIVICCSPSSY 307
                                                                                  4 LDKSKVINSALELLNEV---GIEGLT-----TRKLAQKLGVE------QPTLY 42
                                                                                                                                                              43 WHVKNKRALLDALAIEMLDRHHTHFCPLKGESWQ------DFLRNKAKSFRCALLS 92
                                              45; Gaps
7.7%; Score 83.5; DB 1; Length 963; 25.0%; Pred. No. 3.8; tive 22; Mismatches 74; Indels 45
Query Match '...'
Best Local Similarity 25.0%
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                            | : :||
ERRKCEEE 424
                                                                                                                                                                                                                                                                                                                                  150 EHQVAKEE 157
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> Search completed: June 9, 1999, 13:01:03 Job time: 9122 sec

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OM protein '- protein search, using sw model

June 9, 1999, 13:00:33 ; Search time 28.57 Seconds (without alignments) 399.721 Million cell updates/sec Run on:

US-08-486-814-19 1080 1 MSRLDKSKVINSALELLNEV......FGLELIICGLEKQLKCESGS 207 BLOSUM62 Title: Perfect score: Sequence: Scoring table:

180763 seqs, 55169189 residues Searched:

Database :

sp_organelle:*
sp_phage:*
sp_lant:*
sp_lant:*
: sp_rodent:*
: sp_virus:*
: sp_virus:*
: sp_virus:*
: sp_virus:*
: sp_virus:*
: sp_virus:* SPTREMBL_8:*
1: Sp_fungi:*
2: Sp_human:*
3: Sp_invertebrate:*
4: Sp_mammal:*
5: Sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	059466 haemophilus						034643 bacillus su				7	9				Q51730 pseudomonas	P70477 rattus norv	O88663 rattus norv	homo				0	Q54835 streptococc	Q51516 pseudomonas	Q54719 streptococc	P95100 mycobacteri	7	P96676 bacillus su
ID	059466						034643 034									Q51730 Q	P70477	088663	Q13186	075901	070020	042863	Q54830	054835	051516	054719	P95100	003767	P96676 P9
ngth DB	126 9		242 9													-			2477 2								216 9		198 9
% Query Match Length DB	55.3	13.7	11.5	11.4	8.6	9.6	4.6	9.5	9.1	6.8	8.7	8.7	9.8	8.5	8.5	8.2	8.2						0.8	8.0	0.8	7.8	7.7	7.7	1.7
Score	597	147.5	124.5	123	105.5	103.5	102	66	98.5	96.5	94	93.5	93	91.5	91.5	88	88.5	88.5	86.5	86.5	86.5	98	98	86	86	84	83.5	83	83
Result No.	-	7	٣	4	2	Q	7	80	σ'n	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Q59802 staphylococ	029994 archaeoglob	018399 drosophila	Q91290 pleurodeles	034970 bacillus su	O19126 macaca fasc	O19127 macaca mula	025951 helicobacte	O86852 streptomyce	O53165 mycobacteri	007388 mycobacteri		Q59306 clostridium	P94548 bacillus su	O15087 homo sapien	P79138 cercopithec
059802	029994	018399	091290	034970	019126	019127	025951	086852	053165	007388	090631	059306	P94548	015087	P79138
ο;	14	m	12	σ	4	4	σ	σ	σ	σ	12	6	6	~	4
188	192	405	542	207	285	285	235	215	187	82	1364	190	194	1520	369
7.7	7.6	7.6	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.3	7.3	7.3	7.3
83	82.5	82	81.5	. 81	80.5	80.5	80.5	80.5	80	80	79.5	79	79	78.5	78.5

ALIGNMENTS

																	,0								
X; PRT; 126 AA.	01, CREAT	1. 08, LAST ANNOTATION UPDATE)	S21.	RIA; GAMMA SUBDIVISION; PASTEURELLACEAE;				., CURIALE M.S., HILLEN W., LEVY S.B.;	ated	Tn10-like element in Haemophilus parainfluenzae results from a	SSOI GENE: ;	J. BACIEKTOL. 109:990-994 (1967). -!- SIMILARITY: BELONGS TO THE S21P FAMILY OF RIBOSOMAL PROTEINS.				14541 MW; 107F233B CRC32;	55.3%; Score 597; DB 9; Length 126; 92.0%; Pred. No. 1.3e-45; iive 3; Mismatches 7; Indels 0; Gaps	MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60	MSRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60	DRHITHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFL 120				RY; PRT; 259 AA.	L. 01, CREATED) L. 01, LAST SEQUENCE UPDATE)
PRELIMINARY;	(TREMBLREL.	(TREMBLREL.	L PROTEIN PARAINFLUE	OTEOBACTER		A N MOGE	87137315.	HICKMAN R.K.,	e express:	ement in	the repres	TY BELONG	G148989	1081; HTH	U; Tetk;		vat	KVINSALEL	KVINSALEL	CPLKGESWO	CPLEGESWO	125	125	PRELIMINARY	(TREMBLREL. (TREMBLREL.
59466 59466:	01-NOV-1996 01-NOV-1996	01-NOV-1998	30S RIBOSOMAL PROTEIN S21. HAEMOPHILUS PARAINFLUENZA.	BACTERIA; PROTEOBACTERIA;	HAEMOPHILUS.	[1] SPOIIPNOE EPO		HEUER C., HI	"Constitutiv	Tnl0-like el	mutation in the repressor gene.;;	-I- STMILARI	EMBL: M15539; G148989;	PROSITE; PS0	PFAM; PFU044	RIBOSOMAL PROTEIN SEQUENCE 126 AA	Query Match Best Local Similarity Matches 115; Conser	1 MSRLDKS	1 MSRLDKS	61 DRHHTHF	61 DRHHTHF	121 CQQGF 1	121 ANKVF 1	LT 2 01 Q53901	Q53901; 01-NOV-1996 01-NOV-1996
Q59466 ID Q	점점	DT	OE OS	88	ပ္ပ	RN DD	RX	RA.	RT	RI	1 1	3 5	DR	DR	ב הא	SOW	Our Mar	ογ	QQ	Qy	qq	Οy	QQ	RESULT Q53901 ID Q	SEE

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                        117 LAFLCQQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEE--------RET 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., HUTCHINSON C.R.,
                                                                                                                                                                                                                                                                                                                                                                 58 EMLDRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPT-EKQYETLENQ 116
                                                                                                                                                                                                                                                                                                                                                                                    143 MNLLRSGGLHDELAAYGGDLLSTFVTAEALEQSSRNPGTEQGREQAGVFADQLHGYLKSL 202
                                                                                                                                                                                                                                                                                                         4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDAL----AI 57
                                                                                                                                                                                                                                                                                                                                    31 LTQDRIVVTALGILDAEGLDALSMRRLAQELKTGHASLYAHVGNRDELLDLVFDIVLTEV 90
                                                                                                FERNANDEZ MORENO M.A., CABALLERO J.L., HOPWOOD D.A., MALPARTIDA F., "The act cluster contains regulatory and antibiotic export genes, direct targets for translational control by the blda tRNA gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., YU T.W., TAYLOR M., HOFFMANN D., KIM C.G., ZHANG X., HUTCHINSON C.R.,
                                                                                                                                                                                                                                                      Length 259;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIRMICUTES; ACTINOBACTERIA; PSEUDONOCARDIACEAE;
                           BACTERIA; FIRMICUTES; ACTINOBACTERIA; STREPTOMYCETES; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIM C.G., YU T.W., FRYHLE C., HANDA S., FLOSS H.G., J. BIOL. CHEM. 0:0-0(1998).
                                                                                                                                                                                                                                                 13.7%; Score 147.5; DB 9; 26.0%; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                .06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 PTTDSMPPLLRQA--IELFDHQGAEPAFLFGLELIICGL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 PAT-SFPNLVHLAGPITSLD---SDRRFELGLEIIIAGL 237
                                                                                                                                            Streptomyces.";
CELL 66:769-780(1991).
EBML; M64689: 4455360; -.
PRAM; PF00440; tetR; 1.
SEQUENCE 259 AA; 28268 MW; 16ECA071 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      )570; G2792330; -.
242 AA; 27049 MW; 324EB570 CRC32;
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.0%; Pred. No. 1e-05
Matches 57; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TREMBLREL. 06, 01-JUN-1998 (TREMBLREL. 06, 01-AUG-1998 (TREMBLREL. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMYCOLATOPSIS MEDITERRANEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF040570; G2792330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
            STREPTOMYCES COELICOLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHEM. BIOL. 5:0-0(0002)
                                                                                       91347376.
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                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPRESSOR.
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11.5%; Score 124.5; DB 9; Length 242;

Query Match

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RA MUNSTERS, N. GOAGAWARRA N., MOSZER I., ALBERTINI A.M., ALLONI G., AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S., RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BRIGHEL S.C., BRON S., RA BROUILLETS S., BRUSCHI C.V., CALDWELL B., CAPATEN N.M., CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A., BENDILLET S., BRUSCHI C.V., CALDWELL B., CAPATONO V., CARTER N.M., DENIER R.A., ENTRAN K.D., ERRINGTON Y., FABRET C., FERRARI E., FOULGER D., FRITZ C., EARLERS P., GOSFEGAU A., GALLZZI A., GRANDI G., GUISEPI G., GOSFEGAU A., GOLIGHTLY E.J., GRANDI G., GUISEPI G., GOSFEGAU A., HAIGCH Y., HARGOD C.R., HENDAUT A., HILBERT H., GALGERP P., GOSFEGAU A., GOLIGHTLY E.J., GRANDI G., GUISEPI G., GOSFEGAU S., HOLLO M.F., ITAYA M., JONES L., JONES B., AKAMATRA D., KASAHRA Y., KROGH S., KOWANO M., KURITA K., LAVIDUS R.A KARMATRA D., LAZAREVIC V., LEE S. M., LEVINE A., LIU H., RABUDA S., MAUBL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M., MOSSTL D., NARAI S., NOBACK M., NOONE D., O'RELLY M., OGANA K., OGTWARA A., OUDGEA B., PRAK S.H., PARRO V., POLL T.M., PORTETELLE D., RACHWARA A., OUDGEA B., PRENCILIK S., PRENCILIK S., PRENCILIK S., PRENCILIK S., SELGOLH G., SERON R.A., SEROR S.J., SHOR S.J., SCHROFTER R., SCOFFONE F., SERIGUCHI J., SEKOWSKA A., SEROR S.J., SHOR S., SCHEDLY R.A., TANARA I., TANARAISI H., TAKEWARU K., TAKEWAR T., TAKEWARU R., TAKEW
                            7;
                                                                                                                                                                        EM----LDRHHTHFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSD---TRPTEKQY 110
                                                                                                                                                                                                             111 ETLENQLAFLCQQGFSLENALYALSAVGHFTLGCVLEDQ---EHQV----AKEERETPTT 163
                                                                                                                                                                                                                                                                                                                          138 --TECAQAVMACSPLPLKDRSAALNVVFQYVYGFTATESRWLEHLAETGRTAEEFAAEVT 195
                                                                                                                  27 SELDREKIVATAVRVLDAEGDAKFSMRLLAEELNVTPMSVYWYVANKDDLLELALDAVAG 86
                                                                        SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRAL----LDALAI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECTENCE FROM N.A.
LAPIDUS A., GALLERON N., SOROKIN A., EHRLICH D.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
25.7%; Pred. No. 0.00099;
ive 35; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, 01-NOV-1998 (TREMBLREL. 08,
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSCRIPTION REGULATOR.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           164 DSM 166
                                                                                                                                                                                                                                                                                                                                                                                                                        196 GSM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACILLUS
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                         Matches
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RESULT
034643
                                                                    RESULT
067927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 ----HFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETLENQLAFLC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 CIAODAADAEGGSWTVF-RHTLLHFFERLQSNDIYYKFH--------NILFLKC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 QQGFSLENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSMPPLLRQAIE---LFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 EH--TEONA--AVIAIA------RKHQAIWREKIT-----AVLTEAVENODLAD 155
                                                                                                                                                                                                                                                60 LDRHHTHFCPLKGES------WQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYE 111
                                                                                                                                                                                                                                                                           67 FDQMADSVTERKGDSAMLSLAHAYVDFAIENPGYYEAALL-----KVH-----DKRTE 114
                                                                                                                                                                                                                                                                                                        112 TLENQLAFICQQGFSLENALYALSAVGHFTLG--CVLEDQEHQVAKE--ERETPTTDSMP 167
                                                                                                                                                                                                                                                                                                                                    115 IVSDQIVCLVTK-LLIENGYASEKTAIHATRGLRSLLHGFTVLIAKEAFEREEDILESLS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION; NEISSERIACEAE; NEISSERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 KEHLMLAALETFYRKGIARTSLNEIAQAAGVTRGALYWHFKNKEDLFDALFORICDDIEN 71
                                                                                                                             Query Match 11.4%; Score 123; DB 9; Length 191; Best Local Similarity 24.1%; Pred. No. 0.001; Matches 49; Conservative 38; Mismatches 74; Indels 42; Gaps
                                                                                                                                                                                       4 LDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAI----EM 59
                                                                                                                                                                                                                 7 LIQKMIVDAAAEIADQEGVNGVSLAALSKKMNVRPPSLYNHINGLQAIRAELAVRGLIKL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOL. MICROBIOL. 11:769-775(1994).
-!- SIMILARITY: BELONGS TO THE S21P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.8%; Score 105.5; DB 9; Length 210; 26.8%; Pred. No. 0.039; Live 23; Mismatches 73; Indels 43
 STRAIN=168;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
EMBL, AF027868; G2619045; -.
EMBL, 299114; E1185379; -.
SEQUENCE 191 AA; 21016 MW; CB192356 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CH95 (MULTIPLY ANTIBIOTIC-RESISTANT STRAIN);
MEDLINE; 94254732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 AA; 24218 MW; E2FEDFC3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO1081; "THTTETR_FAMILY; 1. PFAM; PF00440; tetR; 1. RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                    168 PLLRQAIELFDHQGAEPAFLFGL 190
                                                                                                                                                                                                                                                                                                                                                                                                 174 FSIR-----TFLSGL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30S RIBOSOMAL PROTEIN S21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 26.8
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 225796; G438191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEISSERIA GONORRHOEAE
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73 RHKLEVALQRGETDEEILESIVDTLIDYAFSNPESFRFLNLYH------LLKEY 120
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DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEER R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN N.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AEO00776; G2984362; -
PROSITE; PSO1081; HTH_TETR_FAMILY; 1.

PROSITE; PSO1081; HTH_TETR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRARAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; THE COMPLETE GENOME Of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 22.7%; Pred. No. 0.052;
Matches 45; Conservative 35; Mismatches 67; Indels 51.
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL REGULATOR (TETR/ACRR FAMILY).
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BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX
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05,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 YDEETIKKELKKVLKSAI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                         156 DLDKETAVIF 165
179 HQGAEPAFLF 188
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MEDLINE; 98196666
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RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORILLETS R., BRUSCHI C.V., CALDWELL B., CAPUNNO V., CARTER N.M.,
RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUNNO N., CARTER N.M.,
RA BUTTAN K.D., ERRINGTON J., FERRAIT E., FOULGER D., FRITZ C.,
RA FULITA M., FUJITA Y., FUMA S., GALLIZI A., GALLERON N., GHIMS S.Y.,
RA GLASER P., GOFFEAU A., GOLIGHILY E.J., GRANDI G., GUISEPPI G.,
RA HOLSAPPEL S., HOGONO S., HULLO M.F., ITAYA M., JONES I., JORIS B.,
KARRMATA D., KASAHRAA Y., KRARR-BLANCHARD M., KLEIN C., KOBAYASHI Y.,
RA HOLSAPPEL S., HOGONO S., HULLO M.F., ITAYA M., JONES I., JORIS B.,
KARRMATA D., LAZAREUL V., LEE S.M., LEVINE A., LIU H.,
RA AGINARA A., OUDGGA B., PARK S.H., PARKO W., KRITA K., LIU H.,
RA GINARA A., OUDGA B., PARK S.H., PARKO V., POHL T.M., OGAMA K.,
GINARA A., OUDGA B., PARK S.H., PARKO V., POHL T.M., OGAMA K.,
A GINARA A., OUDGA B., PARK S.H., PARKO V., POHL T.M., OGAMA K.,
A GINARA A., OUDGA B., SOROKIN A., TAACONI E., TARAGI T.,
RA SERROR P., SHIN B.S., SOLDO B., SOROKIN B., TARAGI T.,
RARAHASHI H., TAREMARU R., TAKEUCHI M., TAMARASHI H., TAKEMARU R., VANDENDER E.,
RARAHASHI H., TAKEMARU R., TAKEUCHI M., TAMARASHI H., TAKEMARU R., VOSHIDA R., VORNERE E., WEDLER E.,
WANNIER F., VASSAROTI A., VARBIAT R., WANDER E.,
WANNIER F., VASSAROTI A., VARBIAT R., WANDER E.,
WANNIER F., VASSAROTI A., VANDENDER E.,
WANNIER F., VASSAROTI A., VOSHIDA R., YANDENDE E.,
WASSUMOTO K., YATA K., YOSHIDA R., YOSHIRAM A., YONDERLE E.,
WANDER P., SHIR B.S., VOSHIDA R., YONDERLE E.,
WINTER PROMINGER P., WINTERS P., WINTER P., YONDERLE E.,
WANDER P., WANDER P., VOSHIRAM A., YONDERLE E.,
WANDER P., WANDER P., WANDER F., YONGHER E.,
WANDER P., WANDER P., VOSHIRAM A., YONDERLE E.,
WANDER P., WANDER F., VOSHIRAM A., YONDERLE E.,
WANDER P., WANDER F., VOSHIRAM A., YONDER E., WANDER E., WANDER E., WANDER E.,
WANDER P., WANDER F., VOSHIRAM A., YONDER E., WANDER E., 
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BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | :::::|::|| : | | ||:::|:| | : ||::|:|| | : ||::|:|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||:|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||::|| | : ||:|| | : ||:|| | : ||:|| | : | : ||:|| | : ||:|| | : ||:|| | : ||:|| | : ||:|| | : ||:|| | : | : ||:|| | : ||:|| | : ||:|| | : ||:|| | : ||:|| | : ||:|| | : | : ||:|| | : ||:|| | : ||:|| | : || : || : || : || : || : || : |
LAZAREVIC V., SOLDO B., RIVOLTA C., REYNOLDS S., MAUEL C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.4%; Score 102; DB 9; Length 189; 26.6%; Pred. No. 0.069; ative 27; Mismatches 36; Indels
                                                                            SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF017113; G2618838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PUTATIVE TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00440; tetR; 1.
SEQUENCE 189 AA; 21534 MW; 75FBEB90 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 HHTHFCPLKGESWQDFLRNKAKSFRCAL--LSHR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 HSSNRGSILEQTEGDLYKDLLHIGTCLLEELEHR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 299122; E1184426; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.6%
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                    STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTV040.09.
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053789
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62 RHHTHFCPL-KGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTR----PTEKQYETLEN- 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLE S.T.; "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                 PHILIPP W J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARAMAKI H., KOGA H., SAGARA Y., HOSOI M., HORIUCHI T.; "Complete nucleotide sequence of the 5-exo-hydroxycamphor dehydrogenase gene on the CAM plasmid of Pseudomonas putida (ATCC 17453).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASMID CAM.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "camR, a negative regulator locus of the cytochrome P-450cam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOGA H., ARAMAKI H., YAMAGUCHI E., TAKEUCHI K., HORIUCHI T., GUNSALUS I.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.2%; Score 99; DB 9; Length 196; 25.8%; Pred. No. 0.13; tive 27; Mismatches 72; Indels
                                                                                                                                                                                                                     COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.; SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                             HAMLIN N., CHURCHER C.M.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL: AL021943; E1253107; -.
SEQUENCE 196 AA; 21262 MW; 17D86001 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 ----QLAFLCQQGFSLENALYAL----SAVGHFTL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydroxylase operon.";
J. BACIERIOL. 166:1089-1095(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.8%.
Matches 40; Conservative
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96181548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 86223770
MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAM REPRESSOR.
                                                                        STRAIN=H37RV;
                                                                                                                                                                                                   STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                             STRAIN=H37RV
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Q51597;
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66 HFCPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETL--ENQLAF---- 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 DLLCSEKFRNIYFEKIEDAKRRFEKFLEKHFPSKAEILSEIILGFLRQLILHYVIKEERE 156
                                         66 HFCP----LKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTEKQYETL------ 114
                                                                           -----ENQLAFLCQQGFSLENALYAL-------SAVGHF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68; Indels 72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 KERILEVSKELFFEKGYQGTSVEEIVKRANLSKGAFYFHFKSKEELI----TEIIERTHK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 KIISL ------FEENKEKTPEELL -------EMFLEVLYREKKVVYIFLF 96
                                                                                                                                                                        151 TLAMAEMFNNELREMELNRAALELAAFAAFGSAASATEWWLGPEPDSPRRMPREOFVAHL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=VF5;
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDWAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
SUBMITTED (JUL.1997) TO EMEL/GENBANK/DDBJ DATA BANKS.
EMBL; AE000721; G2983549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
32 RNEIVDAAFRAIDRLGPE-LSVRQIAEEAGTAKPKIYRHFTDKSDLLEAIGMRLRDMLWA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 98196666.
DECKERT G., WARKEN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., DECKERT G., WOVERBER R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%; Score 94; DB 9; Length 179;
21.4%; Pred. No. 0.33;
tive 33; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL REGULATOR (TETR/ACRR FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 TPTIDSMPPLLRQAIELFDHQGAEPAFLFGLELIICGLEK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 LP---FLKEKLRE-------GLKLIFEGVKK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21554 MW; E359173B CRC32;
                                                                                                                                                                                                                                                 141 T---LGCVLEDQEHQVAKEERETPTTDSMP--PLLR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                        179 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 21.4% Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NATURE 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQUIFEX AEOLICUS
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P73186;
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P73186
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067157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHT 65
                                                                                             MEDLINE; 94304997.
ARAMAKI H., SAGARA Y., TAKEUCHI K., KOGA H., HORIUCHI T.;
"Nucleotide sequence of the gene encoding a repressor for the
cytochrome P-450cam hydroxylase operon on the Pseudomonas putida CAM
                                                                                                                                                                                                                                                                                                                                                                                                   9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 KSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKN----KRALLDALAIEMLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.9%; Score 96.5; DB 9; Length 246; 18.5%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                      Query Match 9.1%; Score 98.5; DB 9; Length 186; Best Local Similarity 29.8%; Pred. No. 0.14; Matches 25; Conservative 19; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BARRELL B.G., RAJANDREAM M.A., PARKHILL J., COLE S.T.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLIVER K., HARRIS D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.6 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
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EMBL; AL021287; E1237796; -
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 AA; 27618 MW; DC3E2076 CRC32;
                                                                                                                                                                                                                                                                                          SEQUENCE 186 AA; 20438 MW; 56E43196 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Mismatches
           BIOCHIM. BIOPHYS. ACTA 1174:91-94(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 RHH---THFCPLKG--ESWQDFLR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 AYHGGTEERGPLKGIRDGWATFLQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                    EMBL; D14680; G473745; -. PFAM; PF00440; tetk; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 96181548.
PHILIPP W.J., POUI
                                                      SEQUENCE FROM N.A.
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BACILLUS SUBTILIS.
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KANEKO I., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSMWA M., SUGIURA M., SASAMOTO S., KIMURA I.,
HOSOUCHI I., MATSUNO A., MURKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA I., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 CPLKGESWQDFLRNKAKSFRCALLSHRNGAKVHSDTRPTERQYETLENQLAFLCQQGFSL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::: ||:| | | || ||: ||| | : ||: ||:|:| :|
46 RILKGALKLFGTKGYEGTTTKDLAQAANVAEGTLFRYFTNKKAILVEVAT------ 96
                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of the genome of the unicellular cyanobacterium Synchopystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA RES. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 KVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEMLDRHHTHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.7%; Score 93.5; DB 9; Length 236; 22.0%; Pred. No. 0.51; tive 22; Mismatches 59; Indels 43
                       01-NOV-1998 (TREMBLREE. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 26.4 KD PROTEIN.
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
                                                                                                                                                                        TABATA S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; FIRMICUTES; ACTINOBACTERIA; STREPTOMYCETES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEEGER K.J., HARRIS D.;
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 ENALYALSAVGHFTLGCVLEDQEHQVAKEERETPTTDSM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 RENKYLLQV-----CFVEAQYHPELREKIQSEIIDKM 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26384 MW; A8D84E37 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D90904; G1652289; -.
PROSITE: PS01081; HTH_TETR_FAMILY; 1.
PFAM, FF00440; tetR; 1.
HYPOTHETICAL PROTEIN
SEQUENCE 236 AA; 26384 MW; A8D84E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TREMBLREL. 08, CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TREMBLREL. 08, LAST SE
1-NOV-1998 (TREMBLREL. 08, LAST AN
PUTATIVE TRANSCRIPTIONAL REGULATOR.
SC8A6.20C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.03
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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MEDLINE; 97000351.
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26.50.LT
26.20.LT
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MACL. MICROBIOL. 21:77-96(1996).
EMBL; AL031013; E1309426. -.
SEQUENCE 217 AA; 23650 MW; FBFEC38D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIA; FIRMICUTES; ACTINOBACTERIA; MYCOBACTERIA; MYCOBACTERIACEAE;
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                3 RLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAIEML 60
                                                                                                                                                                                                                                                                            PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 213;
                                                                                                                                                       Query Match

8.6%; Score 93; DB 9; Length 217;
Best Local Similarity 37.9%; Pred. No. 0.51;
Matches 22; Conservative 11; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "An integrated map of the genome of the tubercle bacillus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLIVER K., HARRIS D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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007001;
01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 22.2 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996)
EMBL; AL021646; E1248751; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL PROTEIN.
SEQUENCE 213 AA; 23120 MW; 2316B357 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.5%; Score 91.5; DE
Best Local Similarity 38.9%; Pred. No. 0.67;
Matches 21; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TREMBLREL. 06, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TREMBLREL. 08, I
HYPOTHETICAL 23.1 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TREMBLREL. 06,
(TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-H37RV
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007001
AC 007001;
DT 01-JUL.
DT 01-NOV.
DE HYPOTHI
OS BACILLI
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RA KUNST E., OGASARARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BROUILLET S., BOURSTER L., BRANS A., BRAUN W., CARTER N.M.,
BROUILLET S., BOUNESTER L., BRANS A., BRAUN W., CARTER N.M.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA BROUILLET S., BERINGTON J., FABRET C., FERRAIL CHS., FOULGER D., FRITZ C.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRAIL CHS., FOULGER D., FRITZ C.,
RA GUTSAR M., FOLITA Y., FUMA S., GALIZZI A., GALIERON N., GHIM S.Y.,
A GOLFARER P., KOSTEGA A., GOLIGHTLY E.J., GRANDI G., GUISEPEI G.,
A HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L., JORIS B.,
A KARAMARA D., KASHARA Y., KLAERR-BLANCHARD M., KURITA K., LAPIDUS A.,
RA ACRIE P., KONINGSTEIN G., KROGH S., KUMANO M., KURITA K., LAPIDUS A.,
RA ANGELL C., MEDIGUE C., MEDIUN N., MELLADO R.P., MIZUNO M.,
MOSULD S., MAUGI C., MEDIGUE C., MEDIUN N., MELLADO R.P., PORNOLLIK S., PRESCOTT A.M., PRESECAN E., PUJIC P., PURNELLE B.,
RA POPORT G., REY M., REYNOLDS S., RIEGER N., RIVOLETA C., ROCHA E.,
RA ROCHE B., ROSE M., SADAIE Y., SAND T., SCANLAN E., SCHREICH B.,
RA TAKAHAGHI H., TAKEMANU K., TAKECH N., TANGAN T.,
RA SERROR P., SHIN B.S., SOLDO B., SORNEIN A., TARCONI E., TANAR T.,
RA TAKAHAGHI H., TAKEMANU K., TAKECH N., TANGAN E.,
RA TAKAHAGHI H., TAKEMANU K., TAKECH N., TANGAN E.,
RA TAKAHAGHI H., TAKEMANU K., TAKECH N., WEBLER E.,
REPSTER P., VASSAROTTI A., VIRRIA A., YAMANE R.,
RA TAKAHAGHI H., TAKEMANU K., TAKECH N., WANDITR R., WEBLER R.,
RA HULLSENGGER T., WINTERS P., WIPAT A., YAMANE R.,
RASUMOTO K., YATA K., YOSHIRAMA H.F., ZUNGTEIN E.,
RA HULLSENDEGER T., WINTERS P., WIPAT A., YAMANER R.,
RASUMOTO K., YATA K., YOSHIRAMA H.E., ZUNGTEIN E.,
RA HULLSENDE C., WIPAT A., WIPAT A., YAHAMOTO H., YAMANE R.,
ROBICHE W., WIPAT S.,
RA HULLSHAMAN H., DANCHIN A.;
THE COMPLETE WE OFFICE OF THE WANDIEL RESULT OF THE WIPAT SUMBLING RESULL THE COMPLICATION BOLILUS.
THE COMPLETE WE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.5%; Score 91.5; DB 9; Length 194; 22.6%; Pred. No. 0.6; tive 30; Mismatches 36; Indels 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 294043; E313126; -.
EMBL; 299121; E1186136; -.
PFAM: PFO0440; tetR; 1.
SEQUENCE 194 AA: 22227 MW; D3457AEC CRC32;
                                                                                                                        SUBMITIED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 22.6
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 390:249-256(1997).
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103 VLCYSGLAIDHSM 115
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                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                         MEDLINE; 98044033
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                                                                                                                                                                                               STRAIN=168
                              BACILLUS
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Search completed: June 9, 1999, 13:00:33 Job time: 9152 sec

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